



#4

SEQUENCE LISTING

<110> Kinsella, Todd

<120> IN VIVO PRODUCTION OF CYCLIC PEPTIDES

<130> A-68614-1/DJB/RMS/RMK

<140> US 09/800,770

<141> 2001-03-06

<150> US 60/187,130

<151> 2000-03-06

<160> 90

<170> PatentIn version 3.1

<210> 1

<211> 431

<212> PRT

<213> Synechocystis PCC6803

<400> 1

Gly Cys Ile Ser Gly Asp Ser Leu Ile Ser Leu Ala Ser Thr Gly Lys
1 5 10 15

Arg Val Ser Ile Lys Asp Leu Leu Asp Glu Lys Asp Phe Glu Ile Trp
20 25 30

Ala Ile Asn Glu Gln Thr Met Lys Leu Glu Ser Ala Lys Val Ser Arg
35 40 45

Val Phe Cys Thr Gly Lys Lys Leu Val Tyr Ile Leu Lys Thr Arg Leu
50 55 60

Gly Arg Thr Ile Lys Ala Thr Ala Asn His Arg Phe Leu Thr Ile Asp
65 70 75 80

Gly Trp Lys Arg Leu Asp Glu Leu Ser Leu Lys Glu His Ile Ala Leu
85 90 95

Pro Arg Lys Leu Glu Ser Ser Ser Leu Gln Leu Met Ser Asp Glu Glu
100 105 110

Leu Gly Leu Leu Gly His Leu Ile Gly Asp Gly Cys Thr Leu Pro Arg
115 120 125

His Ala Ile Gln Tyr Thr Ser Asn Lys Ile Glu Leu Ala Glu Lys Val
 130 135 140

Val Glu Leu Ala Lys Ala Val Phe Gly Asp Gln Ile Asn Pro Arg Ile
 145 150 155 160

Ser Gln Glu Arg Gln Trp Tyr Gln Val Tyr Ile Pro Ala Ser Tyr Arg
 165 170 175

Leu Thr His Asn Lys Lys Asn Pro Ile Thr Lys Trp Leu Glu Asn Leu
 180 185 190

Asp Val Phe Gly Leu Arg Ser Tyr Glu Lys Phe Val Pro Asn Gln Val
 195 200 205

Phe Glu Gln Pro Gln Arg Ala Ile Ala Ile Phe Leu Arg His Leu Trp
 210 215 220

Ser Thr Asp Gly Cys Val Lys Leu Ile Val Glu Lys Ser Ser Arg Pro
 225 230 235 240

Val Ala Tyr Tyr Ala Thr Ser Ser Glu Lys Leu Ala Lys Asp Val Gln
 245 250 255

Ser Leu Leu Leu Lys Leu Gly Ile Asn Ala Arg Leu Ser Lys Ile Ser
 260 265 270

Gln Asn Gly Lys Gly Arg Asp Asn Tyr His Val Thr Ile Thr Gly Gln
 275 280 285

Ala Asp Leu Gln Ile Phe Val Asp Gln Ile Gly Ala Val Asp Lys Asp
 290 295 300

Lys Gln Ala Ser Val Glu Glu Ile Lys Thr His Ile Ala Gln His Gln
 305 310 315 320

Ala Asn Thr Asn Arg Asp Val Ile Pro Lys Gln Ile Trp Lys Thr Tyr
 325 330 335

Val Leu Pro Gln Ile Gln Ile Lys Gly Ile Thr Thr Arg Asp Leu Gln
 340 345 350

Met Arg Leu Gly Asn Ala Tyr Cys Gly Thr Ala Leu Tyr Lys His Asn

355

360

365

Leu Ser Arg Glu Arg Ala Ala Lys Ile Ala Thr Ile Thr Gln Ser Pro
 370 375 380

Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile Tyr Trp Asp Ser Ile Val
 385 390 395 400

Ser Ile Thr Glu Thr Gly Val Glu Glu Val Phe Asp Leu Thr Val Pro
 405 410 415

Gly Pro His Asn Phe Val Ala Asn Asp Ile Ile Val His Asn Ser
 420 425 430

<210> 2
 <211> 200
 <212> PRT
 <213> Mycobacterium xenopi

<400> 2

Tyr Cys Ile Thr Gly Asp Ala Leu Val Ala Leu Pro Glu Gly Glu Ser
 1 5 10 15

Val Arg Ile Ala Asp Ile Val Pro Gly Ala Arg Pro Asn Ser Asp Asn
 20 25 30

Ala Ile Asp Leu Lys Val Leu Asp Arg His Gly Asn Pro Val Leu Ala
 35 40 45

Asp Arg Leu Phe His Ser Gly Glu His Pro Val Tyr Thr Val Arg Thr
 50 55 60

Val Glu Gly Leu Arg Val Thr Gly Thr Ala Asn His Pro Leu Leu Cys
 65 70 75 80

Leu Val Asp Val Ala Gly Val Pro Thr Leu Leu Trp Lys Leu Ile Asp
 85 90 95

Glu Ile Lys Pro Gly Asp Tyr Ala Val Ile Gln Arg Ser Ala Phe Ser
 100 105 110

Val Asp Cys Ala Gly Phe Ala Arg Gly Lys Pro Glu Phe Ala Pro Thr
 115 120 125

Thr Tyr Thr Val Gly Val Pro Gly Leu Val Arg Phe Leu Glu Ala His
 130 135 140

His Arg Asp Pro Asp Ala Gln Ala Ile Ala Asp Glu Leu Thr Asp Gly
 145 150 155 160

Arg Phe Tyr Tyr Ala Lys Val Ala Ser Val Thr Asp Ala Gly Val Gln
 165 170 175

Pro Val Tyr Ser Leu Arg Val Asp Thr Ala Asp His Ala Phe Ile Thr
 180 185 190

Asn Gly Phe Val Ser His Asn Thr
 195 200

<210> 3
 <211> 458
 <212> PRT
 <213> Chlamydomonas eugametos

<400> 3

Glu Cys Leu Thr Ser Asp His Thr Val Leu Thr Thr Arg Gly Trp Ile
 1 5 10 15

Pro Ile Ala Asp Val Thr Leu Asp Asp Lys Val Ala Val Leu Asp Asn
 20 25 30

Asn Thr Gly Glu Met Ser Tyr Gln Asn Pro Gln Lys Val His Lys Tyr
 35 40 45

Asp Tyr Glu Gly Pro Met Tyr Glu Val Lys Thr Ala Gly Val Asp Leu
 50 55 60

Phe Val Thr Pro Asn His Arg Met Tyr Val Asn Thr Thr Asn Asn Thr
 65 70 75 80

Thr Asn Gln Asn Tyr Asn Leu Val Glu Ala Ser Ser Ile Phe Gly Lys
 85 90 95

Lys Val Arg Tyr Lys Asn Asp Ala Ile Trp Asn Lys Thr Asp Tyr Gln
 100 105 110

Phe Ile Leu Pro Glu Thr Ala Thr Leu Thr Gly His Thr Asn Lys Ile

[illegible]

Ser Gln Lys Ile Asn Lys Asn Thr Leu Val Leu Thr Lys Asn Asn Val
 355 360 365

Lys Ser Gln Thr Met His Ser Gln Arg Ala Glu Arg Val Asp Thr Ala
 370 375 380

Leu Leu Thr Gln Lys Glu Leu Asp Asn Ser Leu Asn His Glu Ile Leu
 385 390 395 400

Ile Asn Lys Asn Pro Gly Thr Ser Gln Leu Glu Cys Val Val Asn Pro
 405 410 415

Glu Val Asn Asn Thr Ser Thr Asn Asp Arg Phe Val Tyr Tyr Lys Gly
 420 425 430

Pro Val Tyr Cys Leu Thr Gly Pro Asn Asn Val Phe Tyr Val Gln Arg
 435 440 445

Asn Gly Lys Ala Val Trp Thr Gly Asn Ser
 450 455

<210> 4
 <211> 341
 <212> PRT
 <213> Chilo iridescent virus

<400> 4

Leu Cys Val Ala Pro Glu Thr Met Ile Leu Thr Glu Asp Gly Gln Phe
 1 5 10 15

Pro Ile Lys Asp Leu Glu Gly Lys Ile Ile Lys Val Trp Asn Gly Asn
 20 25 30

Glu Phe Ser Ser Val Thr Val Val Lys Thr Gly Thr Glu Lys Glu Leu
 35 40 45

Leu Glu Val Glu Leu Ser Asn Gly Cys Thr Leu Ser Cys Thr Pro Glu
 50 55 60

His Lys Phe Ile Ile Val Lys Ser Tyr Thr Glu Ala Lys Lys Gln Lys
 65 70 75 80

Thr Asp Asp Asn Ala Ile Ala Asn Ala Glu Arg Val Asp Ala Gln Asp
 85 90 95

Leu Lys Pro Arg Met Lys Leu Ile Lys Phe Asp Leu Pro Thr Leu Phe
 100 105 110

Gly Asn Ser Glu His Asp Ile Lys Tyr Pro Tyr Thr His Gly Phe Phe
 115 120 125

Cys Gly Asp Gly Thr Tyr Thr Lys Tyr Gly Lys Pro Gln Leu Ser Leu
 130 135 140

Tyr Gly Asp Lys Lys Glu Leu Leu Thr Tyr Leu Asp Val Arg Thr Met
 145 150 155 160

Thr Gly Leu Glu Asp Ala Ser Gly Arg Leu Asn Thr Trp Leu Pro Leu
 165 170 175

Asp Leu Ala Pro Lys Phe Asp Val Pro Ile Asn Ser Ser Leu Glu Cys
 180 185 190

Arg Met Glu Trp Leu Ala Gly Tyr Leu Asp Ala Asp Gly Cys Val Phe
 195 200 205

Arg Asn Gly Thr Asn Glu Ser Ile Gln Val Ser Cys Ile His Leu Asp
 210 215 220

Phe Leu Lys Arg Ile Gln Leu Leu Leu Ile Gly Met Gly Val Thr Ser
 225 230 235 240

Lys Ile Thr Lys Leu His Asp Glu Lys Ile Thr Thr Met Pro Asp Gly
 245 250 255

Lys Gly Gly Gln Lys Pro Tyr Ser Cys Lys Pro Ile Trp Arg Leu Phe
 260 265 270

Ile Ser Ser Ser Gly Leu Tyr His Leu Ser Glu Gln Gly Phe Glu Thr
 275 280 285

Arg Arg Leu Lys Trp Glu Pro Arg Gln Pro Gln Arg Asn Ala Glu Arg
 290 295 300

Phe Val Glu Val Leu Lys Val Asn Lys Thr Gly Arg Val Asp Asp Thr

305

310

315

320

Tyr Cys Phe Thr Glu Pro Ile Asn His Ala Gly Val Phe Asn Gly Ile
 325 330 335

Leu Thr Gly Gln Cys
 340

<210> 5

<211> 473

<212> PRT

<213> Candida tropicalis

<400> 5

Gly Cys Phe Thr Lys Gly Thr Gln Val Met Met Ala Asp Gly Ala Asp
 1 5 10 15

Lys Ser Ile Glu Ser Ile Glu Val Gly Asp Lys Val Met Gly Lys Asp
 20 25 30

Gly Met Pro Arg Glu Val Val Gly Leu Pro Arg Gly Tyr Asp Asp Met
 35 40 45

Tyr Lys Val Arg Gln Leu Ser Ser Thr Arg Arg Asn Ala Lys Ser Glu
 50 55 60

Gly Leu Met Asp Phe Thr Val Ser Ala Asp His Lys Leu Ile Leu Lys
 65 70 75 80

Thr Lys Gln Asp Val Lys Ile Ala Thr Arg Lys Ile Gly Gly Asn Thr
 85 90 95

Tyr Thr Gly Val Thr Phe Tyr Val Leu Glu Lys Thr Lys Thr Gly Ile
 100 105 110

Glu Leu Val Lys Ala Lys Thr Lys Val Phe Gly His His Ile His Gly
 115 120 125

Gln Asn Gly Ala Glu Glu Lys Ala Ala Thr Phe Ala Ala Gly Ile Asp
 130 135 140

Ser Lys Glu Tyr Ile Asp Trp Ile Ile Glu Ala Arg Asp Tyr Val Gln
 145 150 155 160

Val Asp Glu Ile Val Lys Thr Ser Thr Thr Gln Met Ile Asn Pro Val
165 170 175

His Phe Glu Ser Gly Lys Leu Gly Asn Trp Leu His Glu His Lys Gln
180 185 190

Asn Lys Ser Leu Ala Pro Gln Leu Gly Tyr Leu Leu Gly Thr Trp Ala
195 200 205

Gly Ile Gly Asn Val Lys Ser Ser Ala Phe Thr Met Asn Ser Lys Asp
210 215 220

Asp Val Lys Leu Ala Thr Arg Ile Met Asn Tyr Ser Ser Lys Leu Gly
225 230 235 240

Met Thr Cys Ser Ser Thr Glu Ser Gly Glu Leu Asn Val Ala Glu Asn
245 250 255

Glu Glu Glu Phe Phe Asn Asn Leu Gly Ala Glu Lys Asp Glu Ala Gly
260 265 270

Asp Phe Thr Phe Asp Glu Phe Thr Asp Ala Met Asp Glu Leu Thr Ile
275 280 285

Asn Val His Gly Ala Ala Ala Ser Lys Lys Asn Asn Leu Leu Trp Asn
290 295 300

Ala Leu Lys Ser Leu Gly Phe Arg Ala Lys Ser Thr Asp Ile Val Lys
305 310 315 320

Ser Ile Pro Gln His Ile Ala Val Asp Asp Ile Val Val Arg Glu Ser
325 330 335

Leu Ile Ala Gly Leu Val Asp Ala Ala Gly Asn Val Glu Thr Lys Ser
340 345 350

Asn Gly Ser Ile Glu Ala Val Val Arg Thr Ser Phe Arg His Val Ala
355 360 365

Arg Gly Leu Val Lys Ile Ala His Ser Leu Gly Ile Glu Ser Ser Ile
370 375 380

Asn Ile Lys Asp Thr His Ile Asp Ala Ala Gly Val Arg Gln Glu Phe
 385 390 395 400

Ala Cys Ile Val Asn Leu Thr Gly Ala Pro Leu Ala Gly Val Leu Ser
 405 410 415

Lys Cys Ala Leu Ala Arg Asn Gln Thr Pro Val Val Lys Phe Thr Arg
 420 425 430

Asp Pro Val Leu Phe Asn Phe Asp Leu Ile Lys Ser Ala Lys Glu Asn
 435 440 445

Tyr Tyr Gly Ile Thr Leu Ala Glu Glu Thr Asp His Gln Phe Leu Leu
 450 455 460

Ser Asn Met Ala Leu Val His Asn Cys
 465 470

<210> 6
 <211> 162
 <212> PRT
 <213> Guillardia theta

<400> 6

Gly Cys Leu Ser Tyr Ala Thr Asn Gln Pro Tyr Phe Leu Lys Ser Asp
 1 5 10 15

Asn Val Asn Phe Ser Lys Leu Thr Ser Leu Lys Val Ser Asn His Tyr
 20 25 30

Ile Leu Ser Ala Thr Leu Glu Leu Leu Ile Pro Phe Gln Tyr Asn Arg
 35 40 45

Ile Tyr Pro Ile Val Ser Leu Ile Lys Arg Glu Leu Gln Thr Gly Tyr
 50 55 60

Lys Val Val Tyr Glu Leu Asp Phe Tyr Ile Ser Val Ile Val Ser Thr
 65 70 75 80

Val Glu His Tyr Val Leu Thr Leu Asn Gly Trp Lys Arg Ile Leu Glu
 85 90 95

Leu Thr Val Asp Asp Leu Val Ala Thr Leu Asp Ile Gln Tyr Leu Ile
 100 105 110

Tyr Asn Asn Thr Glu Val Asp Leu Phe Ser Ser Asn Val Ile Phe Ser
 115 120 125

Ser Val Ile Asn Leu Ile Cys Met Asn Arg Ile Asn Val Tyr Asp Phe
 130 135 140

Trp Ile Pro Lys Thr Asn Asn Phe Phe Val Asn Ala Leu Leu Val His
 145 150 155 160

Asn Ser

<210> 7
 <211> 152
 <212> PRT
 <213> Porphyra purpurea

<400> 7

Gly Cys Ile Ser Lys Phe Ser His Ile Met Trp Ser His Val Ser Lys
 1 5 10 15

Pro Leu Phe Asn Phe Ser Ile Lys Lys Ser His Met His Asn Phe Asn
 20 25 30

Lys Asn Ile Tyr Gln Leu Leu Asp Gln Gly Glu Ala Phe Ile Ser Arg
 35 40 45

Gln Asp Lys Lys Thr Thr Tyr Lys Ile Arg Thr Asn Ser Glu Lys Tyr
 50 55 60

Leu Glu Leu Thr Ser Asn His Lys Ile Leu Thr Leu Arg Gly Trp Gln
 65 70 75 80

Arg Cys Asp Gln Leu Leu Cys Asn Asp Met Ile Thr Thr Gln Ile Gly
 85 90 95

Phe Glu Leu Ser Arg Lys Lys Lys Tyr Leu Leu Asn Cys Ile Pro Phe
 100 105 110

Ser Leu Cys Asn Phe Glu Thr Leu Ala Asn Ile Asn Ile Ser Asn Phe
 115 120 125

Gln Asn Val Phe Asp Phe Ala Ala Asn Pro Ile Pro Asn Phe Ile Ala
 130 135 140

Asn Asn Ile Ile Val His Asn Ser
 145 150

<210> 8
 <211> 456
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 8

Gly Cys Phe Ala Lys Gly Thr Asn Val Leu Met Ala Asp Gly Ser Ile
 1 5 10 15

Glu Cys Ile Glu Asn Ile Glu Val Gly Asn Lys Val Met Gly Lys Asp
 20 25 30

Gly Arg Pro Arg Glu Val Ile Lys Leu Pro Arg Gly Arg Glu Thr Met
 35 40 45

Tyr Ser Val Val Gln Lys Ser Gln His Arg Ala His Lys Ser Asp Ser
 50 55 60

Ser Arg Glu Val Pro Glu Leu Leu Lys Phe Thr Cys Asn Ala Thr His
 65 70 75 80

Glu Leu Val Val Arg Thr Pro Arg Ser Val Arg Arg Leu Ser Arg Thr
 85 90 95

Ile Lys Gly Val Glu Tyr Phe Glu Val Ile Thr Phe Glu Met Gly Gln
 100 105 110

Lys Lys Ala Pro Asp Gly Arg Ile Val Glu Leu Val Lys Glu Val Ser
 115 120 125

Lys Ser Tyr Pro Ile Ser Glu Gly Pro Glu Arg Ala Asn Glu Leu Val
 130 135 140

Glu Ser Tyr Arg Lys Ala Ser Asn Lys Ala Tyr Phe Glu Trp Thr Ile
 145 150 155 160

Glu Ala Arg Asp Leu Ser Leu Leu Gly Ser His Val Arg Lys Ala Thr
 165 170 175

Tyr Gln Thr Tyr Ala Pro Ile Leu Tyr Glu Asn Asp His Phe Phe Asp
180 185 190

Tyr Met Gln Lys Ser Lys Phe His Leu Thr Ile Glu Gly Pro Lys Val
195 200 205

Leu Ala Tyr Leu Leu Gly Leu Trp Ile Gly Asp Gly Leu Ser Asp Arg
210 215 220

Ala Thr Phe Ser Val Asp Ser Arg Asp Thr Ser Leu Met Glu Arg Val
225 230 235 240

Thr Glu Tyr Ala Glu Lys Leu Asn Leu Cys Ala Glu Tyr Lys Asp Arg
245 250 255

Lys Glu Pro Gln Val Ala Lys Thr Val Asn Leu Tyr Ser Lys Val Val
260 265 270

Arg Gly Asn Gly Ile Arg Asn Asn Leu Asn Thr Glu Asn Pro Leu Trp
275 280 285

Asp Ala Ile Val Gly Leu Gly Phe Leu Lys Asp Gly Val Lys Asn Ile
290 295 300

Pro Ser Phe Leu Ser Thr Asp Asn Ile Gly Thr Arg Glu Thr Phe Leu
305 310 315 320

Ala Gly Leu Ile Asp Ser Asp Gly Tyr Val Thr Asp Glu His Gly Ile
325 330 335

Lys Ala Thr Ile Lys Thr Ile His Thr Ser Val Arg Asp Gly Leu Val
340 345 350

Ser Leu Ala Arg Ser Leu Gly Leu Val Val Ser Val Asn Ala Glu Pro
355 360 365

Ala Lys Val Asp Met Asn Gly Thr Lys His Lys Ile Ser Tyr Ala Ile
370 375 380

Tyr Met Ser Gly Gly Asp Val Leu Leu Asn Val Leu Ser Lys Cys Ala
385 390 395 400

Gly Ser Lys Lys Phe Arg Pro Ala Pro Ala Ala Ala Phe Ala Arg Glu
 405 410 415

Cys Arg Gly Phe Tyr Phe Glu Leu Gln Glu Leu Lys Glu Asp Asp Tyr
 420 425 430

Tyr Gly Ile Thr Leu Ser Asp Asp Ser Asp His Gln Phe Leu Leu Ala
 435 440 445

Asn Gln Val Val Val His Asn Cys
 450 455

<210> 9
 <211> 366
 <212> PRT
 <213> Mycobacterium flavescens

<400> 9

Gly Cys Phe Ala Tyr Gly Thr Arg Gly Ala Leu Ala Asp Gly Thr Thr
 1 5 10 15

Glu Lys Ile Gly Lys Ile Val Asn Gln Lys Met Asp Val Glu Val Met
 20 25 30

Ser Tyr Asp Pro Asp Thr Asp Gln Val Val Pro Arg Lys Val Val Asn
 35 40 45

Trp Phe Asn Asn Gly Pro Ala Glu Gln Phe Leu Gln Phe Thr Val Glu
 50 55 60

Lys Ser Gly Gly Asn Gly Lys Ser Gln Phe Ala Ala Thr Pro Asn His
 65 70 75 80

Leu Ile Arg Thr Pro Ala Gly Trp Thr Glu Ala Gly Asp Leu Val Ala
 85 90 95

Gly Asp Arg Val Met Ala Ala Glu Pro His Arg Leu Ser Asp Gln Gln
 100 105 110

Phe Gln Val Val Leu Gly Ser Leu Met Gly Asp Gly Asn Leu Ser Pro
 115 120 125

Asn Arg Arg Asp Arg Asn Gly Val Arg Phe Arg Met Gly His Gly Ala

130	135	140															
Lys	Gln	Val	Asp	Tyr	Leu	Gln	Trp	Lys	Thr	Ala	Leu	Leu	Gly	Asn	Ile		
145					150					155					160		
Lys	His	Ser	Thr	His	Val	Asn	Asp	Lys	Gly	Ala	Thr	Phe	Val	Asp	Phe		
				165					170					175			
Thr	Pro	Leu	Pro	Glu	Leu	Ala	Glu	Leu	Gln	Arg	Ala	Val	Tyr	Leu	Gly		
			180					185						190			
Asp	Gly	Lys	Lys	Phe	Leu	Ser	Glu	Glu	Asn	Phe	Lys	Ala	Leu	Thr	Pro		
		195					200					205					
Leu	Ala	Leu	Val	Phe	Trp	Tyr	Met	Asp	Asp	Gly	Pro	Phe	Thr	Val	Arg		
	210					215					220						
Ser	Lys	Gly	Leu	Gln	Glu	Arg	Thr	Ala	Gly	Gly	Ser	Gly	Arg	Ile	Glu		
225				230						235					240		
Ile	Cys	Val	Glu	Ala	Met	Ser	Glu	Gly	Asn	Arg	Ile	Arg	Leu	Arg	Asp		
			245						250					255			
Tyr	Leu	Arg	Asp	Thr	His	Gly	Leu	Asp	Val	Arg	Leu	Arg	Leu	Ser	Gly		
			260					265					270				
Ala	Ala	Gly	Lys	Ser	Val	Leu	Val	Phe	Ser	Thr	Ala	Ser	Ser	Ala	Lys		
		275					280					285					
Phe	Gln	Glu	Leu	Val	Ala	Pro	Tyr	Ile	Thr	Pro	Ser	Met	Glu	Tyr	Lys		
	290					295					300						
Leu	Leu	Pro	Arg	Phe	Arg	Gly	Gln	Gly	Ala	Val	Thr	Pro	Gln	Phe	Val		
305					310					315					320		
Glu	Pro	Thr	Gln	Arg	Leu	Val	Pro	Ala	Arg	Val	Leu	Asp	Val	His	Val		
				325					330					335			
Lys	Pro	His	Thr	Arg	Ser	Met	Asn	Arg	Phe	Asp	Ile	Glu	Val	Glu	Gly		
			340					345					350				
Asn	His	Asn	Tyr	Phe	Val	Asp	Gly	Val	Met	Val	His	Asn	Ser				
		355					360					365					

<210> 10
 <211> 124
 <212> PRT
 <213> Synechocystis PCC6803

<400> 10

Tyr Cys Leu Ser Phe Gly Thr Glu Ile Leu Thr Val Glu Tyr Gly Pro
 1 5 10 15

Leu Pro Ile Gly Lys Ile Val Ser Glu Glu Ile Asn Cys Ser Val Tyr
 20 25 30

Ser Val Asp Pro Glu Gly Arg Val Tyr Thr Gln Ala Ile Ala Gln Trp
 35 40 45

His Asp Arg Gly Glu Gln Glu Val Leu Glu Tyr Glu Leu Glu Asp Gly
 50 55 60

Ser Val Ile Arg Ala Thr Ser Asp His Arg Phe Leu Thr Thr Asp Tyr
 65 70 75 80

Gln Leu Leu Ala Ile Glu Glu Ile Phe Ala Arg Gln Leu Asp Leu Leu
 85 90 95

Thr Leu Glu Asn Ile Lys Gln Thr Glu Glu Ala Leu Asp Asn His Arg
 100 105 110

Leu Pro Phe Pro Leu Leu Asp Ala Gly Thr Ile Lys
 115 120

<210> 11
 <211> 147
 <212> PRT
 <213> Mycobacterium leprae

<400> 11

Lys Ala Leu Ala Leu Asp Thr Pro Leu Pro Thr Pro Thr Gly Trp Thr
 1 5 10 15

Ala Met Gly Asp Val Ala Val Gly Asp Glu Leu Leu Ala Val Asp Glu
 20 25 30

Ala Pro Thr Arg Val Val Ala Ala Thr Glu Val Met Leu Gly Arg Pro

35 40 45
 Cys Tyr Glu Ile Glu Phe Ser Asp Gly Thr Val Ile Val Ala Asp Ala
 50 55 60
 Gln His Gln Trp Pro Thr Ser Tyr Gly Ile Arg Thr Ser Ala Gln Leu
 65 70 75 80
 Arg Cys Gly Leu Asp Ile Ile Ala Ala Ala Gly Ser Thr Pro Arg His
 85 90 95
 Ala Gly Arg Leu Thr Thr Ala Ala Phe Met Ala Pro Val Leu Cys Ile
 100 105 110
 Asp Ser Val Arg Arg Val Arg Ser Val Pro Val Arg Cys Val Glu Val
 115 120 125
 Asp Asn Ala Ala His Leu Tyr Leu Ala Gly Arg Gly Met Val Pro Thr
 130 135 140
 His Asn Ser
 145

 <210> 12
 <211> 170
 <212> PRT
 <213> Methanococcus jannaschii

 <400> 12
 Gly Ala Leu Ala Tyr Asp Glu Pro Ile Tyr Leu Ser Asp Gly Asn Ile
 1 5 10 15
 Ile Asn Ile Gly Glu Phe Val Asp Lys Phe Phe Lys Lys Tyr Lys Asn
 20 25 30
 Ser Ile Lys Lys Glu Asp Asn Gly Phe Gly Trp Ile Asp Ile Gly Asn
 35 40 45
 Glu Asn Ile Tyr Ile Lys Ser Phe Asn Lys Leu Ser Leu Ile Ile Glu
 50 55 60
 Asp Lys Arg Ile Leu Arg Val Trp Arg Lys Lys Tyr Ser Gly Lys Leu
 65 70 75 80

Ile Lys Ile Thr Thr Lys Asn Arg Arg Glu Ile Thr Leu Thr His Asp
85 90 95

His Pro Val Tyr Ile Ser Lys Thr Gly Glu Val Leu Glu Ile Asn Ala
100 105 110

Glu Met Val Lys Val Gly Asp Tyr Ile Tyr Ile Pro Lys Asn Asn Thr
115 120 125

Ile Asn Leu Asp Glu Val Ile Lys Val Glu Thr Val Asp Tyr Asn Gly
130 135 140

His Ile Tyr Asp Leu Thr Val Glu Asp Asn His Thr Tyr Ile Ala Gly
145 150 155 160

Lys Asn Glu Gly Phe Ala Val Ser Asn Cys
165 170

<210> 13
<211> 524
<212> PRT
<213> Pyrococcus furiosus

<400> 13

Gly Ala Leu Tyr Asp Phe Ser Val Ile Gln Leu Ser Asn Gly Arg Phe
1 5 10 15

Val Leu Ile Gly Asp Leu Val Glu Glu Leu Phe Lys Lys Tyr Ala Glu
20 25 30

Lys Ile Lys Thr Tyr Lys Asp Leu Glu Tyr Ile Glu Leu Asn Glu Glu
35 40 45

Asp Arg Phe Glu Val Val Ser Val Ser Pro Asp Leu Lys Ala Asn Lys
50 55 60

His Val Val Ser Arg Val Trp Arg Arg Lys Val Arg Glu Gly Glu Lys
65 70 75 80

Leu Ile Arg Ile Lys Thr Arg Thr Gly Asn Glu Ile Ile Leu Thr Arg
85 90 95

Asn His Pro Leu Phe Ala Phe Ser Asn Gly Asp Val Val Arg Lys Glu

100	105	110
Ala Glu Lys Leu Lys Val Gly Asp Arg Val Ala Val Met Met Arg Pro		
115	120	125
Pro Ser Pro Pro Gln Thr Lys Ala Val Val Asp Pro Ala Ile Tyr Val		
130	135	140
Lys Ile Ser Asp Tyr Tyr Leu Val Pro Asn Gly Lys Gly Met Ile Lys		
145	150	155
Val Pro Asn Asp Gly Ile Pro Pro Glu Lys Ala Gln Tyr Leu Leu Ser		
165	170	175
Val Asn Ser Tyr Pro Val Lys Leu Val Arg Glu Val Asp Glu Lys Leu		
180	185	190
Ser Tyr Leu Ala Gly Val Ile Leu Gly Asp Gly Tyr Ile Ser Ser Asn		
195	200	205
Gly Tyr Tyr Ile Ser Ala Thr Phe Asp Asp Glu Ala Tyr Met Asp Ala		
210	215	220
Phe Val Ser Val Val Ser Asp Phe Ile Pro Asn Tyr Val Pro Ser Ile		
225	230	235
Arg Lys Asn Gly Asp Tyr Thr Ile Val Thr Val Gly Ser Lys Ile Phe		
245	250	255
Ala Glu Met Leu Ser Arg Ile Phe Gly Ile Pro Arg Gly Arg Lys Ser		
260	265	270
Met Trp Asp Ile Pro Asp Val Val Leu Ser Asn Asp Asp Leu Met Arg		
275	280	285
Tyr Phe Ile Ala Gly Leu Phe Asp Ala Asp Gly Tyr Val Asp Glu Asn		
290	295	300
Gly Pro Ser Ile Val Leu Val Thr Lys Ser Glu Thr Val Ala Arg Lys		
305	310	315
Ile Trp Tyr Val Leu Gln Arg Leu Gly Ile Ile Ser Thr Val Ser Arg		
325	330	335

Val Lys Ser Arg Gly Phe Lys Glu Gly Glu Leu Phe Arg Val Ile Ile
340 345 350

Ser Gly Val Glu Asp Leu Ala Lys Phe Ala Lys Phe Ile Pro Leu Arg
355 360 365

His Ser Arg Lys Arg Ala Lys Leu Met Glu Ile Leu Arg Thr Lys Lys
370 375 380

Pro Tyr Arg Gly Arg Arg Thr Tyr Arg Val Pro Ile Ser Ser Asp Met
385 390 395 400

Ile Ala Pro Leu Arg Gln Met Leu Gly Leu Thr Val Ala Glu Leu Ser
405 410 415

Lys Leu Ala Ser Tyr Tyr Ala Gly Glu Lys Val Ser Glu Ser Leu Ile
420 425 430

Arg His Ile Glu Lys Gly Arg Val Lys Glu Ile Arg Arg Ser Thr Leu
435 440 445

Lys Gly Ile Ala Leu Ala Leu Gln Gln Ile Ala Lys Asp Val Gly Asn
450 455 460

Glu Glu Ala Trp Val Arg Ala Lys Arg Leu Gln Leu Ile Ala Glu Gly
465 470 475 480

Asp Val Tyr Trp Asp Glu Val Val Ser Val Glu Glu Val Asp Pro Lys
485 490 495

Glu Leu Gly Ile Glu Tyr Val Tyr Asp Leu Thr Val Glu Asp Asp His
500 505 510

Asn Tyr Val Ala Asn Gly Ile Leu Val Ser Asn Cys
515 520

<210> 14

<211> 136

<212> PRT

<213> Methanobacterium thermoautotrophicum (delta H strain)

<400> 14

Pro Cys Val Ser Gly Asp Thr Ile Val Met Thr Ser Gly Gly Pro Arg
1 5 10 15

Thr Val Ala Glu Leu Glu Gly Lys Pro Phe Thr Ala Leu Ile Arg Gly
20 25 30

Ser Gly Tyr Pro Cys Pro Ser Gly Phe Phe Arg Thr Cys Glu Arg Asp
35 40 45

Val Tyr Asp Leu Arg Thr Arg Glu Gly His Cys Leu Arg Leu Thr His
50 55 60

Asp His Arg Val Leu Val Met Asp Gly Gly Leu Glu Trp Arg Ala Ala
65 70 75 80

Gly Glu Leu Glu Arg Gly Asp Arg Leu Val Met Asp Asp Ala Ala Gly
85 90 95

Glu Phe Pro Ala Leu Ala Thr Phe Arg Gly Leu Arg Gly Ala Gly Arg
100 105 110

Gln Asp Val Tyr Asp Ala Thr Val Tyr Gly Ala Ser Ala Phe Thr Ala
115 120 125

Asn Gly Phe Ile Val His Asn Cys
130 135

<210> 15
<211> 456
<212> PRT
<213> Pyrococuss furiosus

<400> 15

Gly Cys Ile Asp Gly Lys Ala Lys Ile Ile Phe Glu Asn Glu Gly Glu
1 5 10 15

Glu His Leu Thr Thr Met Glu Glu Met Tyr Glu Arg Tyr Lys His Leu
20 25 30

Gly Glu Phe Tyr Asp Glu Glu Tyr Asn Arg Trp Gly Ile Asp Val Ser
35 40 45

Asn Val Pro Ile Tyr Val Lys Ser Phe Asp Pro Glu Ser Lys Arg Val
50 55 60

Val Lys Gly Lys Val Asn Val Ile Trp Lys Tyr Glu Leu Gly Lys Asp
65 70 75 80

Val Thr Lys Tyr Glu Ile Ile Thr Asn Lys Gly Thr Lys Ile Leu Thr
85 90 95

Ser Pro Trp His Pro Phe Phe Val Leu Thr Pro Asp Phe Lys Ile Val
100 105 110

Glu Lys Arg Ala Asp Glu Leu Lys Glu Gly Asp Ile Leu Ile Gly Gly
115 120 125

Met Pro Asp Gly Glu Asp Tyr Lys Phe Ile Phe Asp Tyr Trp Leu Ala
130 135 140

Gly Phe Ile Ala Gly Asp Gly Cys Phe Asp Lys Tyr His Ser His Val
145 150 155 160

Lys Gly His Glu Tyr Ile Tyr Asp Arg Leu Arg Ile Tyr Asp Tyr Arg
165 170 175

Ile Glu Thr Phe Glu Ile Ile Asn Asp Tyr Leu Glu Lys Thr Phe Gly
180 185 190

Arg Lys Tyr Ser Ile Gln Lys Asp Arg Asn Ile Tyr Tyr Ile Asp Ile
195 200 205

Lys Ala Arg Asn Ile Thr Ser His Tyr Leu Lys Leu Leu Glu Gly Ile
210 215 220

Asp Asn Gly Ile Pro Pro Gln Ile Leu Lys Glu Gly Lys Asn Ala Val
225 230 235 240

Leu Ser Phe Ile Ala Gly Leu Phe Asp Ala Glu Gly His Val Ser Asn
245 250 255

Lys Pro Gly Ile Glu Leu Gly Met Val Asn Lys Arg Leu Ile Glu Asp
260 265 270

Val Thr His Tyr Leu Asn Ala Leu Gly Ile Lys Ala Arg Ile Arg Glu
275 280 285

Lys Leu Arg Lys Asp Gly Ile Asp Tyr Val Leu His Val Glu Glu Tyr
 290 295 300

Ser Ser Leu Leu Arg Phe Tyr Glu Leu Ile Gly Lys Asn Leu Gln Asn
 305 310 315 320

Glu Glu Lys Arg Glu Lys Leu Glu Lys Val Leu Ser Asn His Lys Gly
 325 330 335

Gly Asn Phe Gly Leu Pro Leu Asn Phe Asn Ala Phe Lys Glu Trp Ala
 340 345 350

Ser Glu Tyr Gly Val Glu Phe Lys Thr Asn Gly Ser Gln Thr Ile Ala
 355 360 365

Ile Ile Asn Asp Glu Arg Ile Ser Leu Gly Gln Trp His Thr Arg Asn
 370 375 380

Arg Val Ser Lys Ala Val Leu Val Lys Met Leu Arg Lys Leu Tyr Glu
 385 390 395 400

Ala Thr Lys Asp Glu Glu Val Lys Arg Met Leu His Leu Ile Glu Gly
 405 410 415

Leu Glu Val Val Arg His Ile Thr Thr Thr Asn Glu Pro Arg Thr Phe
 420 425 430

Tyr Asp Leu Thr Val Glu Asn Tyr Gln Asn Tyr Leu Ala Gly Glu Asn
 435 440 445

Gly Met Ile Phe Val His Asn Thr
 450 455

<210> 16
 <211> 539
 <212> PRT
 <213> Pyrococcus sp. GB-D

<400> 16

Asn Ser Ile Leu Pro Glu Glu Trp Val Pro Leu Ile Lys Asn Gly Lys
 1 5 10 15

Val Lys Ile Phe Arg Ile Gly Asp Phe Val Asp Gly Leu Met Lys Ala

20

25

30

Asn Gln Gly Lys Val Lys Lys Thr Gly Asp Thr Glu Val Leu Glu Val
 35 40 45

Ala Gly Ile His Ala Phe Ser Phe Asp Arg Lys Ser Lys Lys Ala Arg
 50 55 60

Val Met Ala Val Lys Ala Val Ile Arg His Arg Tyr Ser Gly Asn Val
 65 70 75 80

Tyr Arg Ile Val Leu Asn Ser Gly Arg Lys Ile Thr Ile Thr Glu Gly
 85 90 95

His Ser Leu Phe Val Tyr Arg Asn Gly Asp Leu Val Glu Ala Thr Gly
 100 105 110

Glu Asp Val Lys Ile Gly Asp Leu Leu Ala Val Pro Arg Ser Val Asn
 115 120 125

Leu Pro Glu Lys Arg Glu Arg Leu Asn Ile Val Glu Leu Leu Leu Asn
 130 135 140

Leu Ser Pro Glu Glu Thr Glu Asp Ile Ile Leu Thr Ile Pro Val Lys
 145 150 155 160

Gly Arg Lys Asn Phe Phe Lys Gly Met Leu Arg Thr Leu Arg Trp Ile
 165 170 175

Phe Gly Glu Glu Lys Arg Val Arg Thr Ala Ser Arg Tyr Leu Arg His
 180 185 190

Leu Glu Asn Leu Gly Tyr Ile Arg Leu Arg Lys Ile Gly Tyr Asp Ile
 195 200 205

Ile Asp Lys Glu Gly Leu Glu Lys Tyr Arg Thr Leu Tyr Glu Lys Leu
 210 215 220

Val Asp Val Val Arg Tyr Asn Gly Asn Lys Arg Glu Tyr Leu Val Glu
 225 230 235 240

Phe Asn Ala Val Arg Asp Val Ile Ser Leu Met Pro Glu Glu Glu Leu
 245 250 255

Lys Glu Trp Arg Ile Gly Thr Arg Asn Gly Phe Arg Met Gly Thr Phe
260 265 270

Val Asp Ile Asp Glu Asp Phe Ala Lys Leu Leu Gly Tyr Tyr Val Ser
275 280 285

Glu Gly Ser Ala Arg Lys Trp Lys Asn Gln Thr Gly Gly Trp Ser Tyr
290 295 300

Thr Val Arg Leu Tyr Asn Glu Asn Asp Glu Val Leu Asp Asp Met Glu
305 310 315 320

His Leu Ala Lys Lys Phe Phe Gly Lys Val Lys Arg Gly Lys Asn Tyr
325 330 335

Val Glu Ile Pro Lys Lys Met Ala Tyr Ile Ile Phe Glu Ser Leu Cys
340 345 350

Gly Thr Leu Ala Glu Asn Lys Arg Val Pro Glu Val Ile Phe Thr Ser
355 360 365

Ser Lys Gly Val Arg Trp Ala Phe Leu Glu Gly Tyr Phe Ile Gly Asp
370 375 380

Gly Asp Val His Pro Ser Lys Arg Val Arg Leu Ser Thr Lys Ser Glu
385 390 395 400

Leu Leu Val Asn Gly Leu Val Leu Leu Leu Asn Ser Leu Gly Val Ser
405 410 415

Ala Ile Lys Leu Gly Tyr Asp Ser Gly Val Tyr Arg Val Tyr Val Asn
420 425 430

Glu Glu Leu Lys Phe Thr Glu Tyr Arg Lys Lys Lys Asn Val Tyr His
435 440 445

Ser His Ile Val Pro Lys Asp Ile Leu Lys Glu Thr Phe Gly Lys Val
450 455 460

Phe Gln Lys Asn Ile Ser Tyr Lys Lys Phe Arg Glu Leu Val Glu Asn
465 470 475 480

Gly Lys Leu Asp Arg Glu Lys Ala Lys Arg Ile Glu Trp Leu Leu Asn
485 490 495

Gly Asp Ile Val Leu Asp Arg Val Val Glu Ile Lys Arg Glu Tyr Tyr
500 505 510

Asp Gly Tyr Val Tyr Asp Leu Ser Val Asp Glu Asp Glu Asn Phe Leu
515 520 525

Ala Gly Phe Gly Phe Leu Tyr Ala His Asn Ser
530 535

<210> 17
<211> 391
<212> PRT
<213> Thermococcus hydrothermalis

<400> 17

Asp Ser Val Thr Gly Glu Thr Glu Ile Ile Ile Lys Arg Asn Gly Lys
1 5 10 15

Val Glu Phe Val Ala Ile Glu Glu Leu Phe Gln Arg Val Asp Tyr Arg
20 25 30

Ile Gly Glu Lys Glu Tyr Cys Val Leu Glu Gly Val Glu Ala Leu Thr
35 40 45

Leu Asp Asn Arg Gly Arg Leu Val Trp Lys Ser Val Pro Tyr Val Met
50 55 60

Arg His Arg Thr Asn Lys Arg Ile Tyr Arg Val Trp Phe Thr Asn Ser
65 70 75 80

Trp Tyr Leu Asp Val Thr Glu Asp His Ser Leu Ile Gly Tyr Met Asn
85 90 95

Thr Ser Lys Val Lys Pro Gly Lys Pro Leu Lys Glu Arg Leu Val Glu
100 105 110

Val Lys Pro Gly Glu Leu Gly Glu Ser Val Lys Ser Leu Ile Thr Pro
115 120 125

Asn Arg Ala Ile Ala His Gly Ile Arg Val Asn Pro Ile Ala Val Lys

130	135	140
Leu Trp Glu Leu Ile Gly Leu Leu Val Gly Asp Gly Asn Trp Gly Gly 145 150 155 160		
Gln Ser Asn Trp Ala Lys Tyr Asn Val Gly Leu Ser Leu Gly Leu Asp 165 170 175		
Lys Glu Glu Ile Glu Glu Lys Ile Leu Lys Pro Leu Lys Asn Thr Gly 180 185 190		
Ile Ile Ser Asn Tyr Tyr Asp Lys Ser Lys Lys Gly Asp Val Ser Ile 195 200 205		
Leu Ser Lys Trp Leu Ala Arg Phe Met Val Arg Tyr Phe Lys Asp Glu 210 215 220		
Ser Gly Ser Lys Arg Ile Pro Glu Phe Met Phe Asn Leu Pro Arg Glu 225 230 235 240		
Tyr Ile Glu Ala Phe Leu Arg Gly Leu Phe Ser Ala Asp Gly Thr Val 245 250 255		
Ser Leu Arg Lys Gly Val Pro Glu Val Arg Leu Thr Ser Val Asn Pro 260 265 270		
Glu Leu Ser Ser Ser Val Arg Lys Leu Leu Trp Leu Val Gly Val Ser 275 280 285		
Asn Ser Met Phe Val Glu Thr Asn Pro Asn Arg Tyr Leu Gly Lys Glu 290 295 300		
Ser Gly Thr His Ser Val His Val Arg Ile Lys Asp Lys His Arg Phe 305 310 315 320		
Ala Glu Arg Ile Gly Phe Leu Leu Asp Arg Lys Ala Thr Lys Leu Ser 325 330 335		
Glu Asn Leu Gly Gly His Thr Ser Lys Lys Arg Ala Tyr Lys Tyr Asp 340 345 350		
Phe Asp Leu Val Tyr Pro Lys Lys Val Glu Glu Ile Ala Tyr Asp Gly 355 360 365		

Tyr Val Tyr Asp Ile Glu Val Glu Gly Thr His Arg Phe Phe Ala Asn
 370 375 380

Gly Ile Leu Val His Asn Thr
 385 390

<210> 18
 <211> 389
 <212> PRT
 <213> *Pyrococcus furiosus*

<400> 18

Lys Cys Leu Leu Pro Glu Glu Lys Val Val Leu Pro Glu Ile Gly Leu
 1 5 10 15

Val Thr Leu Arg Glu Leu Phe Glu Leu Ala Asn Glu Val Val Val Lys
 20 25 30

Asp Glu Glu Lys Glu Val Arg Lys Leu Gly Lys Met Leu Thr Gly Val
 35 40 45

Asp Glu Arg Gly Asn Val Lys Leu Leu Asn Ala Leu Tyr Val Trp Arg
 50 55 60

Val Ala His Lys Gly Glu Met Ile Arg Val Lys Val Asn Gly Trp Tyr
 65 70 75 80

Ser Val Thr Val Thr Pro Glu His Pro Phe Leu Thr Asn Arg Gly Trp
 85 90 95

Val Lys Ala Gly Glu Leu Lys Glu Gly Asp Tyr Ile Ala Ile Pro Arg
 100 105 110

Arg Val Tyr Gly Asn Glu Asp Leu Met Lys Phe Ser Lys Ile Ala Lys
 115 120 125

Glu Leu Gly Ile Lys Gly Asp Glu Lys Glu Phe Tyr Leu Ala Gly Ala
 130 135 140

Ser Leu Asp Ile Pro Ile Lys Val Leu Phe Leu Ala Pro Ser Lys Leu
 145 150 155 160

Val Ser Ala Phe Leu Arg Gly Tyr Phe Asp Ala Lys Gly Val Val Arg
165 170 175

Glu Asn Tyr Ile Glu Val Pro Leu Phe Glu Asp Leu Pro Leu Leu Leu
180 185 190

Leu Arg Phe Gly Ile Val Ser Arg Ile Glu Lys Ser Thr Leu Lys Ile
195 200 205

Ser Gly Lys Arg Asn Leu Glu Leu Phe Arg Lys His Val Gly Phe Thr
210 215 220

Asp Ser Glu Lys Ala Lys Ala Leu Asp Glu Leu Ile Ser Lys Ala Lys
225 230 235 240

Glu Ser Glu Arg Tyr Pro Ile Leu Glu Glu Leu Arg Arg Leu Gly Leu
245 250 255

Leu Phe Gly Phe Thr Arg Asn Glu Leu Arg Ile Glu Glu Asn Pro Thr
260 265 270

Tyr Glu Val Leu Met Glu Ile Leu Glu Arg Ile Glu Arg Gly Ser Pro
275 280 285

Asn Leu Ala Glu Lys Ile Ala Val Leu Glu Gly Arg Ile Lys Glu Glu
290 295 300

Asn Tyr Leu Arg Ile Leu Glu Glu Glu Gly Leu Ile Glu Asn Gly Lys
305 310 315 320

Leu Thr Glu Leu Gly Lys Glu Leu Leu Glu Val Trp Arg Asn Arg Glu
325 330 335

Phe Asp Ser Lys Asp Val Asp Tyr Val Arg Asn Ile Val Glu Asn Leu
340 345 350

Val Phe Leu Pro Val Glu Lys Val Glu Arg Ile Glu Tyr Glu Gly Tyr
355 360 365

Val Tyr Asp Val Thr Thr Glu Thr His Asn Phe Val Ala Asn Gly Ile
370 375 380

Leu Val His Asn Thr

385

<210> 19
<211> 476
<212> PRT
<213> Pyrococcus horikoshii OT3

<400> 19

Gln Cys Phe Ser Gly Glu Glu Val Ile Ile Val Glu Lys Gly Lys Asp
1 5 10 15

Arg Lys Val Val Lys Leu Arg Glu Phe Val Glu Asp Ala Leu Lys Glu
20 25 30

Pro Ser Gly Glu Gly Met Asp Gly Asp Ile Lys Val Thr Tyr Lys Asp
35 40 45

Leu Arg Gly Glu Asp Val Arg Ile Leu Thr Lys Asp Gly Phe Val Lys
50 55 60

Leu Leu Tyr Val Asn Lys Arg Glu Gly Lys Gln Lys Leu Arg Lys Ile
65 70 75 80

Val Asn Leu Asp Lys Asp Tyr Trp Leu Ala Val Thr Pro Asp His Lys
85 90 95

Val Phe Thr Ser Glu Gly Leu Lys Glu Ala Gly Glu Ile Thr Glu Lys
100 105 110

Asp Glu Ile Ile Arg Val Pro Leu Val Ile Leu Asp Gly Pro Lys Ile
115 120 125

Ala Ser Thr Tyr Gly Glu Asp Gly Lys Phe Asp Asp Tyr Ile Arg Trp
130 135 140

Lys Lys Tyr Tyr Glu Lys Thr Gly Asn Gly Tyr Lys Arg Ala Ala Lys
145 150 155 160

Glu Leu Asn Ile Lys Glu Ser Thr Leu Arg Trp Trp Thr Gln Gly Ala
165 170 175

Lys Pro Asn Ser Leu Lys Met Ile Glu Glu Leu Glu Lys Leu Asn Leu
180 185 190

Leu Pro Leu Thr Ser Glu Asp Ser Arg Leu Glu Lys Val Ala Ile Ile
 195 200 205

Leu Gly Ala Leu Phe Ser Asp Gly Asn Ile Asp Arg Asn Phe Asn Thr
 210 215 220

Leu Ser Phe Ile Ser Ser Glu Arg Lys Ala Ile Glu Arg Phe Val Glu
 225 230 235 240

Thr Leu Lys Glu Leu Phe Gly Glu Phe Asn Tyr Glu Ile Arg Asp Asn
 245 250 255

His Glu Ser Leu Gly Lys Ser Ile Leu Phe Arg Thr Trp Asp Arg Arg
 260 265 270

Ile Ile Arg Phe Phe Val Ala Leu Gly Ala Pro Val Gly Asn Lys Thr
 275 280 285

Lys Val Lys Leu Glu Leu Pro Trp Trp Ile Lys Leu Lys Pro Ser Leu
 290 295 300

Phe Leu Ala Phe Met Asp Gly Leu Tyr Ser Gly Asp Gly Ser Val Pro
 305 310 315 320

Arg Phe Ala Arg Tyr Glu Glu Gly Ile Lys Phe Asn Gly Thr Phe Glu
 325 330 335

Ile Ala Gln Leu Thr Asp Asp Val Glu Lys Lys Leu Pro Phe Phe Glu
 340 345 350

Glu Ile Ala Trp Tyr Leu Ser Phe Phe Gly Ile Lys Ala Lys Val Arg
 355 360 365

Val Asp Lys Thr Gly Asp Lys Tyr Lys Val Arg Leu Ile Phe Ser Gln
 370 375 380

Ser Ile Asp Asn Val Leu Asn Phe Leu Glu Phe Ile Pro Ile Ser Leu
 385 390 395 400

Ser Pro Ala Lys Arg Glu Lys Phe Leu Arg Glu Val Glu Ser Tyr Leu
 405 410 415

Ala Ala Val Pro Glu Ser Ser Leu Ala Gly Arg Ile Glu Glu Leu Arg
420 425 430

Glu His Phe Asn Arg Ile Lys Lys Gly Glu Arg Arg Ser Phe Ile Glu
435 440 445

Thr Trp Glu Val Val Asn Val Thr Tyr Asn Val Thr Thr Glu Thr Gly
450 455 460

Asn Leu Leu Ala Asn Gly Leu Phe Val Lys Asn Ser
465 470 475

<210> 20
<211> 496
<212> PRT
<213> Methanococcus jannaschii

<400> 20

Leu Cys Leu Thr Pro Asp Thr Tyr Val Val Leu Gly Asp Gly Arg Ile
1 5 10 15

Glu Thr Ile Glu Asp Ile Val Asn Ala Lys Glu Arg Asn Val Leu Ser
20 25 30

Leu Asp Leu Asp Asn Leu Ser Ile Lys Ile Asp Thr Ala Ile Lys Phe
35 40 45

Trp Lys Leu Arg Tyr Asn Gly Asn Leu Ser Lys Ile Thr Leu Ser Asn
50 55 60

Asn Tyr Glu Leu Lys Ala Thr Pro Asp His Cys Leu Leu Val Leu Arg
65 70 75 80

Asp Asn Gln Leu Lys Trp Ile Pro Ala Lys Asp Ile Lys Glu Asn Asp
85 90 95

Tyr Ile Ala Met Pro Phe Asn Tyr Lys Val Glu Arg Lys Pro Ile Ser
100 105 110

Leu Leu Asn Leu Leu Lys Tyr Leu Asp Ile Thr Asp Val Leu Ile Glu
115 120 125

Phe Asp Glu Asn Ser Thr Ile Phe Glu Lys Ile Ala Glu Tyr Ile Arg
130 135 140

Asn Asn Ile Lys Thr Ser Thr Lys Tyr Lys Tyr Leu Arg Asn Arg Arg
 145 150 155 160

Val Pro Leu Lys Tyr Leu Ile Glu Trp Asn Phe Asp Leu Asp Glu Ile
 165 170 175

Glu Lys Glu Ala Lys Tyr Ile Tyr Lys Ser Val Ala Gly Thr Lys Lys
 180 185 190

Ile Pro Leu Phe Lys Leu Asp Glu Arg Phe Trp Tyr Phe Ala Gly Leu
 195 200 205

Val Leu Gly Asp Gly Ser Ile Gln Asp Ser Lys Ile Arg Ile Ala Gln
 210 215 220

Thr Pro Leu Lys Asp Val Lys Ser Ile Leu Asp Glu Thr Phe Pro Phe
 225 230 235 240

Leu His Asn Trp Ile Ser Gly Asn Gln Val Ile Ile Ser Asn Pro Ile
 245 250 255

Ile Ala Glu Ile Leu Glu Lys Leu Gly Met Arg Asn Gly Lys Leu Asn
 260 265 270

Gly Ile Ile Phe Ser Leu Pro Glu Ser Tyr Ile Asn Ala Leu Ile Ala
 275 280 285

Gly Tyr Phe Asp Thr Asp Gly Cys Phe Ser Leu Leu Tyr Asp Lys Lys
 290 295 300

Ala Lys Lys His Asn Leu Arg Met Val Leu Thr Ser Lys Arg Arg Asp
 305 310 315 320

Val Leu Glu Lys Ile Gly Ile Tyr Leu Asn Ser Ile Gly Ile Leu Asn
 325 330 335

Thr Leu His Lys Ser Arg Glu Val Tyr Ser Leu Ile Ile Ser Asn Lys
 340 345 350

Ser Leu Glu Thr Phe Lys Glu Lys Ile Ala Lys Tyr Leu Lys Ile Arg
 355 360 365

Lys Glu Ala Phe Ile Asn Gly Tyr Lys Thr Tyr Lys Lys Glu His Glu
 370 375 380

Glu Arg Phe Glu Cys Asp Leu Leu Pro Val Lys Glu Val Phe Lys Lys
 385 390 395 400

Leu Thr Phe Glu Lys Gly Arg Lys Glu Ile Leu Lys Asp Ser Lys Ile
 405 410 415

His Ile Glu Asn Trp Tyr Lys Glu Lys Thr Asn Asn Ile Pro Arg Glu
 420 425 430

Lys Leu Lys Thr Val Leu Arg Tyr Ala Asn Asn Ser Glu His Lys Glu
 435 440 445

Phe Leu Glu Lys Ile Val Asn Gly Asp Ile Ser Phe Val Arg Val Lys
 450 455 460

Lys Val Glu Asn Ile Pro Tyr Asp Gly Tyr Val Tyr Asp Leu Ser Ile
 465 470 475 480

Lys His Asn Gln Asn Phe Ile Ser Asn Gly Val Ile Ser His Asn Cys
 485 490 495

<210> 21
 <211> 527
 <212> PRT
 <213> Pyrococcus horikoshii OT3

<400> 21

Lys Cys Leu Thr Gly Asp Thr Lys Val Ile Ala Asn Gly Gln Leu Phe
 1 5 10 15

Glu Leu Arg Glu Leu Val Glu Lys Ile Ser Gly Gly Lys Phe Gly Pro
 20 25 30

Thr Pro Val Lys Gly Leu Lys Val Ile Gly Ile Asp Glu Asp Gly Lys
 35 40 45

Leu Arg Glu Phe Glu Val Gln Tyr Val Tyr Lys Asp Lys Thr Glu Arg
 50 55 60

Leu Ile Arg Ile Arg Thr Arg Leu Gly Arg Glu Leu Lys Val Thr Pro

65

70

75

80

Tyr His Pro Leu Leu Val Asn Arg Arg Asn Gly Glu Ile Lys Trp Val
 85 90 95

Lys Ala Glu Glu Leu Lys Pro Gly Asp Lys Leu Ala Val Pro Arg Phe
 100 105 110

Leu Pro Ile Val Thr Gly Glu Asp Pro Leu Ala Glu Trp Leu Gly Tyr
 115 120 125

Phe Leu Gly Gly Gly Tyr Ala Asp Ser Lys Glu Asn Leu Ile Met Phe
 130 135 140

Thr Asn Glu Asp Pro Leu Leu Arg Gln Arg Phe Met Glu Leu Thr Glu
 145 150 155 160

Lys Leu Phe Ser Asp Ala Arg Ile Arg Glu Ile Thr His Glu Asn Gly
 165 170 175

Thr Ser Lys Val Tyr Val Asn Ser Lys Lys Ala Leu Lys Leu Val Asn
 180 185 190

Ser Leu Gly Asn Ala His Ile Pro Lys Glu Cys Trp Arg Gly Ile Arg
 195 200 205

Ser Phe Leu Arg Ala Tyr Phe Asp Cys Asn Gly Gly Val Lys Gly Asn
 210 215 220

Ala Ile Val Leu Ala Thr Ala Ser Lys Glu Met Ser Gln Glu Ile Ala
 225 230 235 240

Tyr Ala Leu Ala Gly Phe Gly Ile Ile Ser Arg Ile Gln Glu Tyr Arg
 245 250 255

Val Ile Ile Ser Gly Ser Asp Asn Val Lys Lys Phe Leu Asn Glu Ile
 260 265 270

Gly Phe Ile Asn Arg Asn Lys Leu Glu Lys Ala Leu Lys Leu Val Lys
 275 280 285

Lys Asp Asp Pro Gly His Asp Gly Leu Glu Ile Asn Tyr Glu Leu Ile
 290 295 300

Ser Tyr Val Lys Asp Arg Leu Arg Leu Ser Phe Phe Asn Asp Lys Arg
 305 310 315 320

Ser Trp Ser Tyr Arg Glu Ala Lys Glu Ile Ser Trp Glu Leu Met Lys
 325 330 335

Glu Ile Tyr Tyr Arg Leu Asp Glu Leu Glu Lys Leu Lys Glu Ser Leu
 340 345 350

Ser Arg Gly Ile Leu Ile Asp Trp Asn Glu Val Ala Lys Arg Ile Glu
 355 360 365

Glu Val Ala Glu Glu Thr Gly Ile Arg Ala Asp Glu Leu Leu Glu Tyr
 370 375 380

Ile Glu Gly Lys Arg Lys Leu Ser Phe Lys Asp Tyr Ile Lys Ile Ala
 385 390 395 400

Lys Val Leu Gly Ile Asp Val Glu His Thr Ile Glu Ala Met Arg Val
 405 410 415

Phe Ala Arg Lys Tyr Ser Ser Tyr Ala Glu Ile Gly Arg Arg Leu Gly
 420 425 430

Thr Trp Asn Ser Ser Val Lys Thr Ile Leu Glu Ser Asn Ala Val Asn
 435 440 445

Val Glu Ile Leu Glu Arg Ile Arg Lys Ile Glu Leu Glu Leu Ile Glu
 450 455 460

Glu Ile Leu Ser Asp Glu Lys Leu Lys Glu Gly Ile Ala Tyr Leu Ile
 465 470 475 480

Phe Leu Ser Gln Asn Glu Leu Tyr Trp Asp Glu Ile Thr Lys Val Glu
 485 490 495

Glu Leu Arg Gly Glu Phe Ile Ile Tyr Asp Leu His Val Pro Gly Tyr
 500 505 510

His Asn Phe Ile Ala Gly Asn Met Pro Thr Val Val His Asn Thr
 515 520 525

<210> 22
 <211> 610
 <212> PRT
 <213> *Pyrococcus abyssi*

<400> 22

Ser Cys Val Thr Gly Asp Thr Lys Val Tyr Thr Pro Asp Glu Arg Glu
 1 5 10 15

Val Lys Ile Arg Asp Phe Met Asn Tyr Phe Glu Asn Gly Leu Ile Lys
 20 25 30

Glu Val Ser Asn Arg Ile Gly Arg Asp Thr Val Ile Ala Ala Val Ser
 35 40 45

Phe Asn Ser Arg Ile Val Gly His Pro Val Tyr Arg Leu Thr Leu Glu
 50 55 60

Ser Gly Arg Ile Ile Glu Ala Thr Gly Asp His Met Phe Leu Thr Pro
 65 70 75 80

Glu Gly Trp Lys Gln Thr Tyr Asp Ile Lys Glu Gly Ser Glu Val Leu
 85 90 95

Val Lys Pro Thr Leu Glu Gly Thr Pro Tyr Glu Pro Asp Pro Arg Val
 100 105 110

Ile Ile Asp Ile Lys Glu Phe Tyr Asn Phe Leu Glu Lys Ile Glu Arg
 115 120 125

Glu His Asn Leu Lys Pro Leu Lys Glu Ala Lys Thr Phe Arg Glu Leu
 130 135 140

Ile Thr Lys Asp Lys Glu Lys Ile Leu Arg Arg Ala Leu Glu Leu Arg
 145 150 155 160

Ala Glu Ile Glu Asn Gly Leu Thr Lys Arg Glu Ala Glu Ile Leu Glu
 165 170 175

Leu Ile Ser Ala Asp Thr Trp Ile Pro Arg Ala Glu Leu Glu Lys Lys
 180 185 190

Ala Arg Ile Ser Arg Thr Arg Leu Asn Gln Ile Leu Gln Arg Leu Glu

195	200	205
Lys Lys Gly Tyr Ile Glu Arg Arg Ile Glu Gly Arg Lys Gln Phe Val		
210	215	220
Arg Lys Ile Arg Asn Gly Lys Ile Leu Arg Asn Ala Met Asp Ile Lys		
225	230	235 240
Arg Ile Leu Glu Glu Glu Phe Gly Ile Lys Ile Ser Tyr Thr Thr Val		
	245	250 255
Lys Lys Leu Leu Ser Gly Asn Val Asp Gly Met Ala Tyr Arg Ile Leu		
	260	265 270
Lys Glu Val Lys Glu Lys Trp Leu Val Arg Tyr Asp Asp Glu Lys Ala		
	275	280 285
Gly Ile Leu Ala Arg Val Val Gly Phe Ile Leu Gly Asp Gly His Leu		
	290	295 300
Ala Arg Asn Gly Arg Ile Trp Phe Asn Ser Ser Lys Glu Glu Leu Glu		
305	310	315 320
Met Leu Ala Asn Asp Leu Arg Lys Leu Gly Leu Lys Pro Ser Glu Ile		
	325	330 335
Ile Glu Arg Asp Ser Ser Ser Glu Ile Gln Gly Arg Lys Val Lys Gly		
	340	345 350
Arg Ile Tyr Met Leu Tyr Val Asp Asn Ala Ala Phe His Ala Leu Leu		
	355	360 365
Arg Phe Trp Lys Val Glu Val Gly Asn Lys Thr Lys Lys Gly Tyr Thr		
	370	375 380
Val Pro Glu Trp Ile Lys Lys Gly Asn Leu Phe Val Lys Arg Glu Phe		
385	390	395 400
Leu Arg Gly Leu Phe Gly Ala Asp Gly Thr Lys Pro Cys Gly Lys Arg		
	405	410 415
Tyr Asn Phe Asn Gly Ile Lys Leu Glu Ile Arg Ala Lys Lys Glu Ser		
	420	425 430

Leu Glu Arg Thr Val Glu Phe Leu Asn Asp Val Ala Asp Leu Leu Arg
 435 440 445

Glu Phe Asp Val Asp Ser Lys Ile Thr Val Ser Pro Thr Lys Glu Gly
 450 455 460

Phe Ile Ile Arg Leu Ile Val Thr Pro Asn Asp Ala Asn Tyr Leu Asn
 465 470 475 480

Phe Leu Thr Arg Val Gly Tyr Ala Tyr Ala Lys Asp Thr Tyr Ala Arg
 485 490 495

Leu Val Gly Glu Tyr Ile Arg Ile Lys Leu Ala Tyr Lys Asn Ile Ile
 500 505 510

Leu Pro Gly Ile Ala Glu Lys Ala Ile Glu Leu Ala Thr Val Thr Asn
 515 520 525

Ser Thr Tyr Ala Ala Lys Val Leu Gly Val Ser Arg Asp Phe Val Val
 530 535 540

Asn Arg Leu Lys Gly Thr Gln Ile Gly Ile Thr Arg Asp Phe Met Thr
 545 550 555 560

Phe Glu Glu Phe Met Lys Glu Arg Val Leu Asn Gly Tyr Val Ile Glu
 565 570 575

Lys Val Ile Lys Lys Glu Lys Leu Gly Tyr Leu Asp Val Tyr Asp Val
 580 585 590

Thr Cys Ala Arg Asp His Ser Phe Ile Ser Asn Gly Leu Val Ser His
 595 600 605

Asn Cys
 610

<210> 23
 <211> 490
 <212> PRT
 <213> Methanococcus jannaschii
 <400> 23

Asn Cys Leu Thr Ser Asn Ser Lys Ile Leu Thr Asp Asp Gly Tyr Tyr
 1 5 10 15
 Ile Lys Leu Glu Lys Leu Lys Glu Lys Leu Asp Leu His Ile Lys Ile
 20 25 30
 Tyr Asn Thr Glu Glu Gly Glu Lys Ser Ser Asn Ile Leu Phe Val Ser
 35 40 45
 Glu Arg Tyr Ala Asp Glu Lys Ile Ile Arg Ile Lys Thr Glu Ser Gly
 50 55 60
 Arg Val Leu Glu Gly Ser Lys Asp His Pro Val Leu Thr Leu Asn Gly
 65 70 75 80
 Tyr Val Pro Met Gly Met Leu Lys Glu Gly Asp Asp Val Ile Val Tyr
 85 90 95
 Pro Tyr Glu Gly Val Glu Tyr Glu Glu Pro Ser Asp Glu Ile Ile Leu
 100 105 110
 Asp Glu Asp Asp Phe Ala Glu Tyr Asp Lys Gln Ile Ile Lys Tyr Leu
 115 120 125
 Lys Asp Arg Gly Leu Leu Pro Leu Arg Met Asp Asn Lys Asn Ile Gly
 130 135 140
 Ile Ile Ala Arg Leu Leu Gly Phe Ala Phe Gly Asp Gly Ser Ile Val
 145 150 155 160
 Lys Glu Asn Gly Asp Arg Glu Arg Leu Tyr Val Ala Phe Tyr Gly Lys
 165 170 175
 Arg Glu Thr Leu Ile Lys Ile Arg Glu Asp Leu Glu Lys Leu Gly Ile
 180 185 190
 Lys Ala Ser Arg Ile Tyr Ser Arg Lys Arg Glu Val Glu Ile Arg Asn
 195 200 205
 Ala Tyr Gly Asp Glu Tyr Thr Ser Leu Cys Glu Asp Asn Ser Ile Lys
 210 215 220
 Ile Thr Ser Lys Ala Phe Ala Leu Phe Met His Lys Leu Gly Met Pro

225		230		235		240
Ile Gly Lys Lys Thr Glu Gln Ile Tyr Lys Ile Pro Glu Trp Ile Lys						
	245		250		255	
Lys Ala Pro Lys Trp Val Lys Arg Asn Phe Leu Ala Gly Leu Phe Gly						
	260		265		270	
Ala Asp Gly Ser Arg Ala Val Phe Lys Asn Tyr Thr Pro Leu Pro Ile						
	275		280		285	
Asn Leu Thr Met Ser Lys Ser Glu Glu Leu Lys Glu Asn Ile Leu Glu						
	290		295		300	
Phe Leu Asn Glu Ile Lys Leu Leu Leu Ala Glu Phe Asp Ile Glu Ser						
305		310		315		320
Met Ile Tyr Glu Ile Lys Ser Leu Asp Gly Arg Val Ser Tyr Arg Leu						
	325		330		335	
Ala Ile Val Gly Glu Glu Ser Ile Lys Asn Phe Leu Gly Arg Ile Asn						
	340		345		350	
Tyr Glu Tyr Ser Gly Glu Lys Lys Val Ile Gly Leu Leu Ala Tyr Glu						
	355		360		365	
Tyr Leu Arg Arg Lys Asp Ile Ala Lys Glu Ile Arg Lys Lys Cys Ile						
	370		375		380	
Lys Arg Ala Lys Glu Leu Tyr Lys Lys Gly Val Thr Val Ser Glu Met						
385		390		395		400
Leu Lys Met Asp Glu Phe Arg Asn Glu Phe Ile Ser Lys Arg Leu Ile						
	405		410		415	
Glu Arg Ala Val Tyr Glu Asn Leu Asp Glu Asp Asp Val Arg Ile Ser						
	420		425		430	
Thr Lys Phe Pro Lys Phe Glu Glu Phe Ile Glu Lys Tyr Gly Val Ile						
	435		440		445	
Gly Gly Phe Val Ile Asp Lys Ile Lys Glu Ile Glu Glu Ile Ser Tyr						
	450		455		460	

Asp Ser Lys Leu Tyr Asp Val Gly Ile Val Ser Lys Glu His Asn Phe
 465 470 475 480

Ile Ala Asn Ser Ile Val Val His Asn Cys
 485 490

<210> 24
 <211> 378
 <212> PRT
 <213> Pyrococcus horikoshii OT3

<400> 24

Lys Cys Val Asp Gly Asp Thr Leu Val Leu Thr Lys Glu Phe Gly Leu
 1 5 10 15

Ile Lys Ile Lys Glu Leu Tyr Glu Lys Leu Asp Gly Lys Gly Arg Lys
 20 25 30

Ile Val Glu Gly Asn Glu Glu Trp Thr Glu Leu Glu Lys Pro Ile Thr
 35 40 45

Val Tyr Gly Tyr Lys Asp Gly Lys Ile Val Glu Ile Lys Ala Thr His
 50 55 60

Val Tyr Lys Gly Val Ser Ser Gly Met Val Glu Ile Arg Thr Arg Thr
 65 70 75 80

Gly Arg Lys Ile Lys Val Thr Pro Ile His Arg Leu Phe Thr Gly Arg
 85 90 95

Val Thr Lys Asp Gly Leu Ile Leu Lys Glu Val Met Ala Met His Val
 100 105 110

Lys Pro Gly Asp Arg Ile Ala Val Val Lys Lys Ile Asp Gly Gly Glu
 115 120 125

Tyr Ile Lys Leu Asp Ser Ser Asn Val Gly Glu Ile Lys Val Pro Glu
 130 135 140

Ile Leu Asn Glu Glu Leu Ala Glu Phe Leu Gly Tyr Leu Met Ala Asn
 145 150 155 160

Gly Thr Leu Lys Ser Gly Ile Ile Glu Ile Tyr Cys Asp Asp Glu Ser
165 170 175

Leu Leu Glu Arg Val Asn Ser Leu Ser Leu Lys Leu Phe Gly Val Gly
180 185 190

Gly Arg Ile Val Gln Lys Val Asp Gly Lys Ala Leu Val Ile Gln Ser
195 200 205

Lys Pro Leu Val Asp Val Leu Arg Arg Leu Gly Val Pro Glu Asp Lys
210 215 220

Lys Val Glu Asn Trp Lys Val Pro Arg Glu Leu Leu Leu Ser Pro Ser
225 230 235 240

Asn Val Val Arg Ala Phe Val Asn Ala Tyr Ile Lys Gly Lys Glu Glu
245 250 255

Val Glu Ile Thr Leu Ala Ser Glu Glu Gly Ala Tyr Glu Leu Ser Tyr
260 265 270

Leu Phe Ala Lys Leu Gly Ile Tyr Val Thr Ile Ser Lys Ser Gly Glu
275 280 285

Tyr Tyr Lys Val Arg Val Ser Arg Arg Gly Asn Leu Asp Thr Ile Pro
290 295 300

Val Glu Val Asn Gly Met Pro Lys Val Leu Pro Tyr Glu Asp Phe Arg
305 310 315 320

Lys Phe Ala Lys Ser Ile Gly Leu Glu Glu Val Ala Glu Asn His Leu
325 330 335

Gln His Ile Ile Phe Asp Glu Val Ile Asp Val Arg Tyr Ile Pro Glu
340 345 350

Pro Gln Glu Val Tyr Asp Val Thr Thr Glu Thr His Asn Phe Val Gly
355 360 365

Gly Asn Met Pro Thr Leu Leu His Asn Thr
370 375

<210> 25

<211> 198
 <212> PRT
 <213> Artificial sequence

<220>
 <223> modified wild-type Ssp DnaB Intien

<400> 25

Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile
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Tyr Trp Asp Ser Ile Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val
 20 25 30

Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile
 35 40 45

Ile Val His Asn Ser Ile Glu Gln Gly Gln Gly Gly Gly Met Ser Met
 50 55 60

Asp Tyr Lys Asp Asp Asp Asp Lys Met Arg Met Leu Glu Gly Gln Ala
 65 70 75 80

Gly Gly Leu Ile Thr Ser Gly Cys Ile Ser Gly Asp Ser Leu Ile Ser
 85 90 95

Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp Leu Leu Asp Glu
 100 105 110

Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys Leu Glu
 115 120 125

Ser Lys Val Ser Arg Val Phe Cys Thr Gly Lys Lys Leu Val Tyr Ile
 130 135 140

Leu Lys Thr Arg Leu Gly Arg Thr Ile Lys Ala Thr Ala Asn His Arg
 145 150 155 160

Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp Glu Leu Ser Leu Lys
 165 170 175

Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser Ser Ser Leu Gln Leu
 180 185 190

Ser Ile His Gly Tyr His
195

<210> 26
<211> 35
<212> PRT
<213> Artificial sequence

<220>
<223> FLAG epitope

<400> 26

Ser Ile Glu Gln Gly Gln Gly Gly Gly Met Ser Met Asp Tyr Lys Asp
1 5 10 15

Asp Asp Asp Lys Met Arg Met Leu Glu Gly Gln Ala Gly Gly Leu Ile
20 25 30

Thr Ser Gly
35

<210> 27
<211> 1467
<212> DNA
<213> Synechocystis PCC6803

<220>
<221> CDS
<222> (739) .. (1338)
<223>

<400> 27
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gtaatcaatt acgggggtcat tagttcatag cccatatatg gagttccgcg ttacataact 120
tacggtaaatt ggcccgctg gctgaccgcc caacgacccc cgcgccattga cgtcaataat 180
gacgtatgtt cccatagtaa cgccaatagg gactttccat tgacgtcaat ggggtggacta 240
tttacggtaa actgcccact tggcagtaca tcaagtgtat catatgccaa gtacgcccc 300
tattgacgtc aatgacggta aatggcccgc ctggcattat gcccagtaca tgaccttacc 360
ggactttcct acttggcagt acatctacgt attagtcacg gctattacca tgggtgatgcg 420
gttttggcag tacatcaatg ggcgtggata gcggtttgac tcacggggat ttccaagtct 480
ccacccatt gacgtcaatg ggagtttgtt ttggcaccaa aatcaacggg actttccaaa 540
atgtcgtaac aactccgcc cattgacgca aatgggcggg aggcgtgtac ggtgggaggt 600

ctatataagc agagctctct ggctaactag agaaccact gcttactggc ttatcgaaat	660
taatacgact cactataggg agaccaagc tggctagtta agcttcctat actaggagat	720
ctgtcgactg gaggaacc atg gag tcc gga tca cca gaa ata gaa aag ttg Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu 1 5 10	771
tct cag agt gat att tac tgg gac tcc atc gtt tct att acg gag act Ser Gln Ser Asp Ile Tyr Trp Asp Ser Ile Val Ser Ile Thr Glu Thr 15 20 25	819
gga gtc gaa gag gtt ttt gat ttg act gtg cca gga cca cat aac ttt Gly Val Glu Glu Val Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe 30 35 40	867
gtc gcc aat gac atc att gtc cat aac agt atc gaa caa ggc cag ggc Val Ala Asn Asp Ile Ile Val His Asn Ser Ile Glu Gln Gly Gln Gly 45 50 55	915
ggc ggc atg tca atg gac tat aaa gat gac gac gat aag atg agg atg Gly Gly Met Ser Met Asp Tyr Lys Asp Asp Asp Asp Lys Met Arg Met 60 65 70 75	963
ctc gag ggc caa gca ggt gga ctg atc acc agt ggc tgc atc agt gga Leu Glu Gly Gln Ala Gly Gly Leu Ile Thr Ser Gly Cys Ile Ser Gly 80 85 90	1011
gat agt ttg atc agc ttg gcg agc aca gga aaa aga gtt tct att aaa Asp Ser Leu Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys 95 100 105	1059
gat ttg tta gat gaa aaa gat ttt gaa ata tgg gca att aat gaa cag Asp Leu Leu Asp Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln 110 115 120	1107
acg atg aag cta gaa tca gct aaa gtt agt cgt gta ttt tgt act ggc Thr Met Lys Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly 125 130 135	1155
aaa aag cta gtt tat att tta aaa act cga cta ggt aga act atc aag Lys Lys Leu Val Tyr Ile Leu Lys Thr Arg Leu Gly Arg Thr Ile Lys 140 145 150 155	1203
gca aca gca aat cat aga ttt tta act att gat ggt tgg aaa aga tta Ala Thr Ala Asn His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu 160 165 170	1251
gat gag cta tct tta aaa gag cat att gct cta ccc cgt aaa cta gaa Asp Glu Leu Ser Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu 175 180 185	1299
agc tcc tct tta caa tta atc gat cca tgg tta cca tga caattggcgg Ser Ser Ser Leu Gln Leu Ile Asp Pro Trp Leu Pro 190 195	1348

ccgctcgagt ctagagggcc cgcggttcga aggtaagcct atccctaacc ctctcctcgg 1408

tctcgattct acgcgtaccg gtcacatca ccacacacat tgagtttaaa cccgctgat 1467

<210> 28

<211> 199

<212> PRT

<213> Synechocystis PCC6803

<400> 28

Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile
1 5 10 15

Tyr Trp Asp Ser Ile Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val
20 25 30

Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile
35 40 45

Ile Val His Asn Ser Ile Glu Gln Gly Gln Gly Gly Gly Met Ser Met
50 55 60

Asp Tyr Lys Asp Asp Asp Asp Lys Met Arg Met Leu Glu Gly Gln Ala
65 70 75 80

Gly Gly Leu Ile Thr Ser Gly Cys Ile Ser Gly Asp Ser Leu Ile Ser
85 90 95

Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp Leu Leu Asp Glu
100 105 110

Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys Leu Glu
115 120 125

Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys Lys Leu Val Tyr
130 135 140

Ile Leu Lys Thr Arg Leu Gly Arg Thr Ile Lys Ala Thr Ala Asn His
145 150 155 160

Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp Glu Leu Ser Leu
165 170 175

Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser Ser Ser Leu Gln

Leu Ile Asp Pro Trp Leu Pro
195

<210> 29
<211> 1314
<212> DNA
<213> Synechocystis PCC6803

<400> 29
atggagtcgc gatcaccaga aatagaaaag ttgtctcaga gtgatattta ctgggactcc 60
atcgttttcta ttacggagac tggagtcgaa gaggtttttg atttgactgt gccagggccc 120
cataactttg tggccaatga catcattgtc cataacagtg aggaggacct gggatccagc 180
gtgcagctcg ccgaccacta ccagcagaac acccccatcg gcgacggccc cgtgctgctg 240
cccgacaacc actacctgag caccagtcg gccctgagca aagaccccaa cgagaagcgc 300
gatcacatgg tcctgctgga gttcgtgacc gccgccggga tcactctcgg catggacgag 360
ctgtacaagg ggtcgaacgg ggaattctcg caggtagaca agtcgatggg gagcaagggc 420
gaggagctgt tcaccggggg ggtgcccatc ctggctcgagc tggacggcga cgtaaaccggc 480
cacaagttca gcgtgtccgg cgagggcgag ggcgatgcca cctacggcaa gctgaccctg 540
aagttcatct gcaccaccgg caagctgccc gtgccctggc ccaccctcgt gaccaccctg 600
acctacggcg tgcagtgttt cagccgctac cccgaccaca tgaagcagca cgactttctc 660
aagtcgcgca tgcccgaagg ctacgtccag gagcgcacca tcttcttcaa ggacgacggc 720
aactacaaga cccgcgccga ggtgaagttc gagggcgaca ccctggtgaa ccgcatcgag 780
ctgaagggca tcgacttcaa ggaggacggc aacatcctgg ggcacaagct ggagtacaac 840
tacaacagcc acaacgtcta tatcatggcc gacaagcaga agaacggcat caaggtgaac 900
ttcaagatcc gccacaacat cgaggacctc gagcaaaagc tgatatgcat ctccggaaat 960
agtttgatca gcttggcgag cacaggaaaa agagtttcta ttaaagattt gttagatgaa 1020
aaagattttg aaatatgggc aattaatgaa cagacgatga agctagaatc agctaaagtt 1080
agtcgtgtat tttgtactgg caaaaagcta gtttatattt taaaaactcg actaggtaga 1140
actatcaagg caacagcaaa tcatagattt ttaactattg atgggttgaa aagattagat 1200
gagctatctt taaaagagca tattgctcta ccccgtaaac tagaaagctc ctctttacaa 1260
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<210> 30
 <211> 438
 <212> PRT
 <213> Synechocystis PCC6803

<400> 30

Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile
 1 5 10 15

Tyr Trp Asp Ser Ile Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val
 20 25 30

Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile
 35 40 45

Ile Val His Asn Ser Glu Glu Asp Leu Gly Ser Ser Val Gln Leu Ala
 50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 65 70 75 80

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
 85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
 100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Gly Ser Asn Gly Glu
 115 120 125

Phe Ser Gln Val Asp Lys Ser Met Val Ser Lys Gly Glu Glu Leu Phe
 130 135 140

Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly
 145 150 155 160

His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly
 165 170 175

Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro
 180 185 190

Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser

195	200	205
Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met 210 215 220		
Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly 225 230 235 240		
Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val 245 250 255		
Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile 260 265 270		
Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile 275 280 285		
Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg 290 295 300		
His Asn Ile Glu Asp Leu Glu Gln Lys Leu Ile Cys Ile Ser Gly Asn 305 310 315 320		
Ser Leu Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp 325 330 335		
Leu Leu Asp Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr 340 345 350		
Met Lys Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys 355 360 365		
Lys Leu Val Tyr Ile Leu Lys Thr Arg Leu Gly Arg Thr Ile Lys Ala 370 375 380		
Thr Ala Asn His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp 385 390 395 400		
Glu Leu Ser Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser 405 410 415		
Ser Ser Leu Gln Leu Gly Leu Arg Gly Gln Tyr Pro Tyr Asp Val Pro 420 425 430		

Asp Tyr Ala Ile Asp Glx
435

<210> 31
<211> 1314
<212> DNA
<213> Synechocystis PCC6803

<400> 31
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atcgtttcta ttacggagac tggagtcgaa gaggtttttg atttgactgt gccagggccc 120
cataactttg tggccaatga catcattgtc cataacagtg aggaggacct gggatccagc 180
gtgcagctcg ccgaccacta ccagcagaac acccccatcg gcgacggccc cgtgctgctg 240
cccgacaacc actacctgag caccagtcgc gccctgagca aagaccccaa cgagaagcgc 300
gatcacatgg tcctgctgga gttcgtgacc gccgccggga tcaactctcg catggacgag 360
ctgtacaagg ggtcgaacgg ggaattctcg caggtagaca agtcgatggg gagcaagggc 420
gaggagctgt tcaccggggg ggtgcccatc ctggtcgagc tggacggcga cgtaaacggc 480
cacaagttca gcgtgtccgg cgagggcgag ggcgatgcca cctacggcaa gctgaccctg 540
aagttcatct gcaccaccgg caagctgccc gtgccctggc ccaccctcgt gaccaccctg 600
acctacggcg tgcagtgtt cagccgctac cccgaccaca tgaagcagca cgacttcttc 660
aagtccgcca tgcccgaagg ctacgtccag gagcgcacca tcttcttcaa ggacgacggc 720
aactacaaga cccgcgccga ggtgaagttc gagggcgaca ccctggtgaa ccgcatcgag 780
ctgaagggca tcgacttcaa ggaggacggc aacatcctgg ggcacaagct ggagtacaac 840
tacaacagcc acaacgtcta tatcatggcc gacaagcaga agaacggcat caaggtgaac 900
ttcaagatcc gccacaacat cgaggacctc gagcaaaagc tgatatgcat ctccggaaat 960
agtttgatca gcttggcgag cacaggaaaa agagtttcta ttaaagattt gttagatgaa 1020
aaagattttg aaatatgggc aattaatgaa cagacgatga agctagaatc agctaaagtt 1080
agtcgtgtat tttgtactgg caaaaagcta gtttatattt taaaaactcg actaggtaga 1140
actatcaagg caacagcaaa tcataaattt ttaactattg atggttggaa aagattagat 1200
gagctatctt taaaagagca tattgtctta ccccgtaaag tagaaagctc ctctttacaa 1260
ttaggcctcc gcggccagta cccctacgac gtcccggact acgctatcga ttaa 1314

<210> 32
 <211> 438
 <212> PRT
 <213> Synechocystis PCC6803

<400> 32

Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile
 1 5 10 15

Tyr Trp Asp Ser Ile Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val
 20 25 30

Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile
 35 40 45

Ile Val His Asn Ser Glu Glu Asp Leu Gly Ser Ser Val Gln Leu Ala
 50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 65 70 75 80

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
 85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
 100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Gly Ser Asn Gly Glu
 115 120 125

Phe Ser Gln Val Asp Lys Ser Met Val Ser Lys Gly Glu Glu Leu Phe
 130 135 140

Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly
 145 150 155 160

His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly
 165 170 175

Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro
 180 185 190

Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser
 195 200 205

Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met
 210 215 220

Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly
 225 230 235 240

Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val
 245 250 255

Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile
 260 265 270

Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile
 275 280 285

Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg
 290 295 300

His Asn Ile Glu Asp Leu Glu Gln Lys Leu Ile Cys Ile Ser Gly Asn
 305 310 315 320

Ser Leu Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp
 325 330 335

Leu Leu Asp Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr
 340 345 350

Met Lys Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys
 355 360 365

Lys Leu Val Tyr Ile Leu Lys Thr Arg Leu Gly Arg Thr Ile Lys Ala
 370 375 380

Thr Ala Asn His Lys Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp
 385 390 395 400

Glu Leu Ser Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser
 405 410 415

Ser Ser Leu Gln Leu Gly Leu Arg Gly Gln Tyr Pro Tyr Asp Val Pro
 420 425 430

Asp Tyr Ala Ile Asp Glx
435

<210> 33
<211> 1314
<212> DNA
<213> Synechocystis PCC6803

<400> 33
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atcgtttcta ttacggagac tggagtcgaa gaggtttttg atttgactgt gccagggccc 120
cataactttg tggccaatga catcattgtc cataacagtg aggaggacct gggatccagc 180
gtgcagctcg ccgaccacta ccagcagaac acccccatcg gcgacggccc cgtgctgctg 240
cccgacaacc actacctgag caccagtcgc gccctgagca aagaccccaa cgagaagcgc 300
gatcacatgg tctgctgga gtctgtgacc gccgccggga tcaactctcg catggacgag 360
ctgtacaagg ggtcgaacgg ggaattctcg caggtagaca agtcgatggg gagcaagggc 420
gaggagctgt tcaccggggg ggtgcccatc ctggtcgagc tggacggcga cgtaaacggc 480
cacaagttca gcgtgtccgg cgagggcgag ggcgatgcca cctacggcaa gctgacctg 540
aagttcatct gcaccaccgg caagctgccc gtgccctggc ccacctcgt gaccacctg 600
acctacggcg tgcagtgtt cagccgctac cccgaccaca tgaagcagca cgacttcttc 660
aagtccgcca tgcccgaagg ctacgtccag gagcgcacca tcttcttcaa ggacgacggc 720
aactacaaga cccgcgccga ggtgaagttc gagggcgaca ccctggtgaa ccgcatcgag 780
ctgaagggca tcgacttcaa ggaggacggc aacatcctgg ggcacaagct ggagtacaac 840
tacaacagcc acaacgtcta tatcatggcc gacaagcaga agaacggcat caaggtgaac 900
ttcaagatcc gccacaacat cgaggacctc gagcaaaagc tgatatgcat ctccggaat 960
agtttgatca gcttggcgag cacaggaaaa agagtttcta ttaaagattt gttagatgaa 1020
aaagattttg aaatatgggc agttaatgaa cagacgatga agctagaatc agctaaagtt 1080
agtcgtgtat tttgtactgg caaaaagcta gtttatattt taaaaactcg actaggtaga 1140
actatcaagg caacagcaaa tcatagattt ttaactattg atggttgga aagattagat 1200
gagctatctt taaaagagca tattgtctta ccccgtaaag tagaaagctc ctctttacaa 1260
ttaggcctcc gcggccagta cccctacgac gtcccggact acgctatcga ttaa 1314

<210> 34

<211> 438
 <212> PRT
 <213> Synechocystis PCC6803

<400> 34

Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile
 1 5 10 15

Tyr Trp Asp Ser Ile Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val
 20 25 30

Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile
 35 40 45

Ile Val His Asn Ser Glu Glu Asp Leu Gly Ser Ser Val Gln Leu Ala
 50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 65 70 75 80

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
 85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
 100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Gly Ser Asn Gly Glu
 115 120 125

Phe Ser Gln Val Asp Lys Ser Met Val Ser Lys Gly Glu Glu Leu Phe
 130 135 140

Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly
 145 150 155 160

His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly
 165 170 175

Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro
 180 185 190

Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser
 195 200 205

Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met
 210 215 220

Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly
 225 230 235 240

Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val
 245 250 255

Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile
 260 265 270

Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile
 275 280 285

Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg
 290 295 300

His Asn Ile Glu Asp Leu Glu Gln Lys Leu Ile Cys Ile Ser Gly Asn
 305 310 315 320

Ser Leu Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp
 325 330 335

Leu Leu Asp Glu Lys Asp Phe Glu Ile Trp Ala Val Asn Glu Gln Thr
 340 345 350

Met Lys Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys
 355 360 365

Lys Leu Val Tyr Ile Leu Lys Thr Arg Leu Gly Arg Thr Ile Lys Ala
 370 375 380

Thr Ala Asn His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp
 385 390 395 400

Glu Leu Ser Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser
 405 410 415

Ser Ser Leu Gln Leu Gly Leu Arg Gly Gln Tyr Pro Tyr Asp Val Pro
 420 425 430

Asp Tyr Ala Ile Asp Glx
435

<210> 35
<211> 1314
<212> DNA
<213> Synechocystis PCC6803

<400> 35
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cataactttg tggccaatga catcattgtc cataacagtg aggaggacct gggatccagc 180
gtgcagctcg ccgaccacta ccagcagaac acccccatcg gcgacggccc cgtgctgctg 240
cccgacaacc actacctgag caccagtcgc gccctgagca aagaccccaa cgagaagcgc 300
gatcacatgg tctgctgga gtctgtgacc gccgcgggga tcaactctcg catggacgag 360
ctgtacaagg ggtcgaacgg ggaattctcg caggtagaca agtcgatggt gagcaagggc 420
gaggagctgt tcaccggggt ggtgcccac cttggtcgagc tggacggcga cgtaaacggc 480
cacaagttca gcgtgtccgg cgagggcgag ggcgatgcca cctacggcaa gctgaccctg 540
aagttcatct gcaccaccgg caagctgccc gtgccctggc ccaccctcgt gaccaccctg 600
acctacggcg tgcagtgtt cagccgctac cccgaccaca tgaagcagca cgacttcttc 660
aagtccgcca tgcccgaagg ctacgtccag gagcgacca tcttcttcaa ggacgacggc 720
aactacaaga cccgcgccga ggtgaagttc gagggcgaca ccctggtgaa ccgcatcgag 780
ctgaagggca tcgacttcaa ggaggacggc aacatcctgg ggcacaagct ggagtacaac 840
tacaacagcc acaacgtcta tatcatggcc gacaagcaga agaacggcat caaggtgaac 900
ttcaagatcc gccacaacat cgaggacctc gagcaaaagc tgatatgcat ctccggaaat 960
agtttgatca gcttggcgag cacaggaaaa agagtttcta ttaaagattt gttagatgaa 1020
aaagattttg aaatatgggc aattaatgaa cagacgatga agctagaatc agctaaagtt 1080
agtcgtgtat tttgtactgg caaaaagcta gtttatattt taaaaactcg actaggtaga 1140
actatcaagg caacagcaaa tcatagattt ttaactattg atggttgga aagattagat 1200
gagctatctt taaaagagca tattgtctta ccccgtaaac tagaaagctc ctctttacaa 1260
ttaggcctcc gcggccagta ccctacgac gtcccgact acgctatcga ttaa 1314

<210> 36
<211> 438

<212> PRT

<213> Synechocystis PCC6803

<400> 36

Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile
1 5 10 15

Tyr Trp Asp Ser Ile Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val
20 25 30

Phe Asp Leu Ala Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile
35 40 45

Ile Val His Asn Ser Glu Glu Asp Leu Gly Ser Ser Val Gln Leu Ala
50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65 70 75 80

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Gly Ser Asn Gly Glu
115 120 125

Phe Ser Gln Val Asp Lys Ser Met Val Ser Lys Gly Glu Glu Leu Phe
130 135 140

Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly
145 150 155 160

His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly
165 170 175

Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro
180 185 190

Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser
195 200 205

Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met
 210 215 220
 Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly
 225 230 235 240
 Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val
 245 250 255
 Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile
 260 265 270
 Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile
 275 280 285
 Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg
 290 295 300
 His Asn Ile Glu Asp Leu Glu Gln Lys Leu Ile Cys Ile Ser Gly Asn
 305 310 315 320
 Ser Leu Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp
 325 330 335
 Leu Leu Asp Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr
 340 345 350
 Met Lys Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys
 355 360 365
 Lys Leu Val Tyr Ile Leu Lys Thr Arg Leu Gly Arg Thr Ile Lys Ala
 370 375 380
 Thr Ala Asn His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp
 385 390 395 400
 Glu Leu Ser Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser
 405 410 415
 Ser Ser Leu Gln Leu Gly Leu Arg Gly Gln Tyr Pro Tyr Asp Val Pro
 420 425 430
 Asp Tyr Ala Ile Asp Glx

<210> 37
 <211> 1314
 <212> DNA
 <213> Synechocystis PCC6803

<400> 37
 atggagtcg gatcaccaga aatagaaaag ttgtctcaga gtgatattta ctgggactcc 60
 atcgttcccta ttacggagac tggagtcgaa gaggtttttg atttgactgt gccagggccc 120
 cataactttg tggccaatga catcattgtc cataacagtg aggaggacct gggatccagc 180
 gtgcagctcg ccgaccacta ccagcagaac acccccatcg gcgacggccc cgtgctgctg 240
 cccgacaacc actacctgag caccagtcgc gccctgagca aagaccccaa cgagaagcgc 300
 gatcacatgg tcctgctgga gttcgtgacc gccgcgggga tcaactctcg catggacgag 360
 ctgtacaagg ggtcgaacgg ggaattctcg caggtagaca agtcgatggg gagcaagggc 420
 gaggagctgt tcaccggggg ggtgcccacg ctggtcgagc tggacggcga cgtaaacggc 480
 cacaagttca gcgtgtccgg cgagggcgag ggcgatgcca cctacggcaa gctgaccctg 540
 aagttcatct gcaccaccgg caagctgccc gtgccttggc ccacctcgt gaccacctg 600
 acctacggcg tgcagtgtt cagccgctac cccgaccaca tgaagcagca cgacttcttc 660
 aagtccgcca tgcccgaagg ctacgtccag gagcgcacca tcttcttcaa ggacgacggc 720
 aactacaaga cccgcgccga ggtgaagttc gagggcgaca ccctggtgaa ccgcatcgag 780
 ctgaagggca tcgacttcaa ggaggacggc aacatcctgg ggcacaagct ggagtacaac 840
 tacaacagcc acaacgtcta tatcatggcc gacaagcaga agaacggcat caaggtgaac 900
 ttcaagatcc gccacaacat cgaggacctc gagcaaaagc tgatatgcat ctccggaaat 960
 agtttgatca gcttggcgag cacaggaaaa agagtttcta ttaaagattt gttagatgaa 1020
 aaagattttg aaatatgggc aattaatgaa cagacgatga agctagaatc agctaaagtt 1080
 agtcgtgtat tttgtactgg caaaaagcta gtttatattt taaaaactcg actaggtaga 1140
 actatcaagg caacagcaaa tcatagattt ttaactattg atggttggaa aagattagat 1200
 gagctatctt taaaagagca tattgctcta ccccgtaaag tagaaagctc ctctttacaa 1260
 ttaggcctcc gcggccagta ccctacgac gtcccggact acgctatcga ttaa 1314

<210> 38
 <211> 438
 <212> PRT

<213> Synechocystis PCC6803

<400> 38

Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile
1 5 10 15

Tyr Trp Asp Ser Ile Val Pro Ile Thr Glu Thr Gly Val Glu Glu Val
20 25 30

Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile
35 40 45

Ile Val His Asn Ser Glu Glu Asp Leu Gly Ser Ser Val Gln Leu Ala
50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65 70 75 80

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Gly Ser Asn Gly Glu
115 120 125

Phe Ser Gln Val Asp Lys Ser Met Val Ser Lys Gly Glu Glu Leu Phe
130 135 140

Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly
145 150 155 160

His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly
165 170 175

Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro
180 185 190

Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser
195 200 205

Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met

210	215	220
Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly		
225	230	235 240
Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val		
	245	250 255
Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile		
	260	265 270
Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile		
	275	280 285
Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg		
	290	295 300
His Asn Ile Glu Asp Leu Glu Gln Lys Leu Ile Cys Ile Ser Gly Asn		
305	310	315 320
Ser Leu Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp		
	325	330 335
Leu Leu Asp Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr		
	340	345 350
Met Lys Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys		
	355	360 365
Lys Leu Val Tyr Ile Leu Lys Thr Arg Leu Gly Arg Thr Ile Lys Ala		
	370	375 380
Thr Ala Asn His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp		
385	390	395 400
Glu Leu Ser Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser		
	405	410 415
Ser Ser Leu Gln Leu Gly Leu Arg Gly Gln Tyr Pro Tyr Asp Val Pro		
	420	425 430
Asp Tyr Ala Ile Asp Glx		
435		

<210> 39
 <211> 1314
 <212> DNA
 <213> Synechocystis PCC6803

<400> 39
 atggagtccg gatcaccaga aatagaaaag ttgtctcaga gtgatattta ctgggactcc 60
 atcgttttcta ttacggagac tggagtcgaa gaggtttttg atttgactgt gccagggccc 120
 cataactttg tggccaatga catcattgtc cataacagtg aggaggacct gggatccagc 180
 gtgcagctcg ccgaccacta ccagcagaac acccccatcg gcgacggccc cgtgctgctg 240
 cccgacaacc actacctgag caccagtcg gccctgagca aagaccccaa cgagaagcgc 300
 gatcacatgg tcttctgctgga gttcgtgacc gccgccggga tcaactctcg catggacgag 360
 ctgtacaagg ggtcgaacgg ggaattctcg caggtagaca agtcgatggg gagcaagggc 420
 gaggagctgt tcaccggggg ggtgcccac cttggtcgagc tggacggcga cgtaaacggc 480
 cacaagttca gcgtgtccgg cgagggcgag ggcgatgcca cctacggcaa gctgaccctg 540
 aagttcatct gcaccaccgg caagctgccc gtgccctggc ccacctcgt gaccaccctg 600
 acctacggcg tgcagtgtt cagccgctac cccgaccaca tgaagcagca cgacttcttc 660
 aagtccgcca tgcccgaagg ctacgtccag gagcgcacca tcttcttcaa ggacgacggc 720
 aactacaaga cccgcgccga ggtgaagttc gagggcgaca ccctggtgaa ccgcatcgag 780
 ctgaagggca tcgacttcaa ggaggacggc aacatcctgg ggcacaagct ggagtacaac 840
 tacaacagcc acaacgtcta tatcatggcc gacaagcaga agaacggcat caaggtgaac 900
 ttcaagatcc gccacaacat cgaggacctc gagcaaaagc tgatatgcat ctccggaaat 960
 agtttgatca gcttggcgag cacaggaaaa agagtttcta ttaaagattt gttagatgaa 1020
 aaagattttg aaatatgggc aattaatgaa cagacgatga agctagaatc agctaaagtt 1080
 agtcgtgtat tttgtactgg caaaaggcta gtttatattt taaaaactcg actaggtaga 1140
 actatcaagg caacagcaaa tcatagattt ttaactattg atggttggaa aagattagat 1200
 gagctatctt taaaagagca tattgtctta ccccgtaaac tagaaagctc ctctttacaa 1260
 ttaggcctcc gcggccagta cccctacgac gtcccgact acgctatcga ttaa 1314

<210> 40
 <211> 438
 <212> PRT
 <213> Synechocystis PCC6803

<400> 40

Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile
1 5 10 15

Tyr Trp Asp Ser Ile Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val
20 25 30

Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile
35 40 45

Ile Val His Asn Ser Glu Glu Asp Leu Gly Ser Ser Val Gln Leu Ala
50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65 70 75 80

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Gly Ser Asn Gly Glu
115 120 125

Phe Ser Gln Val Asp Lys Ser Met Val Ser Lys Gly Glu Glu Leu Phe
130 135 140

Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly
145 150 155 160

His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly
165 170 175

Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro
180 185 190

Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser
195 200 205

Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met
210 215 220

Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly
 225 230 235 240

Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val
 245 250 255

Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile
 260 265 270

Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile
 275 280 285

Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg
 290 295 300

His Asn Ile Glu Asp Leu Glu Gln Lys Leu Ile Cys Ile Ser Gly Asn
 305 310 315 320

Ser Leu Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp
 325 330 335

Leu Leu Asp Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr
 340 345 350

Met Lys Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys
 355 360 365

Arg Leu Val Tyr Ile Leu Lys Thr Arg Leu Gly Arg Thr Ile Lys Ala
 370 375 380

Thr Ala Asn His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp
 385 390 395 400

Glu Leu Ser Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser
 405 410 415

Ser Ser Leu Gln Leu Gly Leu Arg Gly Gln Tyr Pro Tyr Asp Val Pro
 420 425 430

Asp Tyr Ala Ile Asp Glx
 435

<210> 41
 <211> 1314
 <212> DNA
 <213> Synechocystis PCC6803

<400> 41
 atggagtcg gatcaccaga aatagaaaag ttgtctcaga gtgatattta ctgggactcc 60
 atcgtttcta ttacggagac tggagtcgaa gaggtttttg atttgactgt gccagggccc 120
 cataactttg tggccaatga catcattgtc cataacagtg aggaggacct gggatccagc 180
 gtgcagctcg ccgaccacta ccagcagaac acccccatcg gcgacggccc cgtgctgctg 240
 cccgacaacc actacctgag caccagtcg gccctgagca aagaccccaa cgagaagcgc 300
 gatcacatgg tcctgctgga gttcgtgacc gccgcggga tcaactctcg catggacgag 360
 ctgtacaagg ggtcgaacgg ggaattctcg caggtagaca agtcgatggg gagcaagggc 420
 gaggagctgt tcaccggggg ggtgcccatc ctggtcgagc tggacggcga cgtaaacggc 480
 cacaagttca gcgtgtccgg cgagggcgag ggcgatgcca cctacggcaa gctgaccctg 540
 aagttcatct gcaccaccgg caagctgccc gtgccctggc ccacctcgt gaccacctg 600
 acctacggcg tgcagtgtt cagccgtac cccgaccaca tgaagcagca cgacttcttc 660
 aagtccgcca tgcccgaagg ctacgtccag gagcgcacca tcttcttcaa ggacgacggc 720
 aactacaaga cccgcgccga ggtgaagttc gaggggcaga ccctggtgaa ccgcatcgag 780
 ctgaagggca tcgacttcaa ggaggacggc aacatcctgg ggcacaagct ggagtacaac 840
 tacaacagcc acaacgtcta tatcatggcc gacaagcaga agaacggcat caaggtgaac 900
 ttcaagatcc gccacaacat cgaggacctc gagcaaaagc tgatatgcat ctccggagat 960
 agtttgatca gcttggcgag cacaggaaaa agagtttcta ttaaagattt gttagatgaa 1020
 aaagattttg aaatatggc aattaatgaa cagacgatga agctagaatc agctaaagtt 1080
 agtcgtgtat tttgtactgg caaaaagcta gtttatattt taaaaactcg actaggtaga 1140
 actatcaagg caacagcaaa tcataaattt ttaactattg atggttggaa aagattagat 1200
 gagctatctt taaaagagca tattgtctta cccgtaaac tagaaagctc ctctttacaa 1260
 ttaggcctcc gcggccagta cccctacgac gtcccgact acgctatcga ttaa 1314

<210> 42
 <211> 438
 <212> PRT
 <213> Synechocystis PCC6803

<400> 42

Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile
1 5 10 15

Tyr Trp Asp Ser Ile Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val
20 25 30

Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile
35 40 45

Ile Val His Asn Ser Glu Glu Asp Leu Gly Ser Ser Val Gln Leu Ala
50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
65 70 75 80

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Gly Ser Asn Gly Glu
115 120 125

Phe Ser Gln Val Asp Lys Ser Met Val Ser Lys Gly Glu Glu Leu Phe
130 135 140

Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly
145 150 155 160

His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly
165 170 175

Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro
180 185 190

Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser
195 200 205

Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met
210 215 220

Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly
 225 230 235 240

Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val
 245 250 255

Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile
 260 265 270

Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile
 275 280 285

Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg
 290 295 300

His Asn Ile Glu Asp Leu Glu Gln Lys Leu Ile Cys Ile Ser Gly Asp
 305 310 315 320

Ser Leu Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp
 325 330 335

Leu Leu Asp Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr
 340 345 350

Met Lys Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys
 355 360 365

Lys Leu Val Tyr Ile Leu Lys Thr Arg Leu Gly Arg Thr Ile Lys Ala
 370 375 380

Thr Ala Asn His Lys Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp
 385 390 395 400

Glu Leu Ser Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser
 405 410 415

Ser Ser Leu Gln Leu Gly Leu Arg Gly Gln Tyr Pro Tyr Asp Val Pro
 420 425 430

Asp Tyr Ala Ile Asp Glx
 435

<210> 43
 <211> 1314
 <212> DNA
 <213> Synechocystis PCC6803

<400> 43
 atggagtcg gatcaccaga aatagaaaag ttgtctcaga gtgatattta ctgggactcc 60
 atcgttccta ttacggagac tggagtcgaa gaggtttttg atttgactgt gccagggccc 120
 cataactttg tggccaatga catcattgtc cataacagtg aggaggacct gggatccagc 180
 gtgcagctcg ccgaccacta ccagcagaac acccccatcg gcgacggccc cgtgctgctg 240
 cccgacaacc actacctgag caccagtcgc gccctgagca aagaccccaa cgagaagcgc 300
 gatcacatgg tcctgctgga gtctgtgacc gccgcgggga tcaactctcg catggacgag 360
 ctgtacaagg ggtcgaacgg ggaattctcg caggtagaca agtcgatggg gagcaagggc 420
 gaggagctgt tcaccggggg ggtgcccacg ctggtcgagc tggacggcga cgtaaacggc 480
 cacaagttca gcgtgtccgg cgagggcgag ggcgatgcca cctacggcaa gctgacctg 540
 aagttcatct gcaccaccgg caagctgccc gtgccctggc ccacctcgt gaccacctg 600
 acctacggcg tgcagtgtt cagccgctac cccgaccaca tgaagcagca cgacttcttc 660
 aagtccgcca tgcccgaagg ctacgtccag gagcgcacca tcttcttcaa ggacgacggc 720
 aactacaaga cccgcgccga ggtgaagttc gagggcgaca ccctggtgaa ccgcatcgag 780
 ctgaagggca tcgacttcaa ggaggacggc aacatcctgg ggcacaagct ggagtacaac 840
 tacaacagcc acaacgtcta tatcatggcc gacaagcaga agaacggcat caaggtgaac 900
 ttcaagatcc gccacaacat cgaggacctc gagcaaaagc tgatatgcat ctccggagat 960
 agtttgatca gcttggcgag cacaggaaaa agagtttcta ttaaagattt gttagatgaa 1020
 aaagattttg aaatatgggc aattaatgaa cagacgatga agctagaatc agctaaagtt 1080
 agtcgtgtat tttgtactgg caaaaagcta gtttatattt taaaaactcg actaggtaga 1140
 actatcaagg caacagcaaa tcatagattt ttaactattg atggttggaa aagattagat 1200
 gagctatctt taaaagagca tattgctcta ccccgtaaac tagaaagctc ctctttacaa 1260
 ttaggcctcc gcggccagta ccctacgac gtcccgact acgctatcga ttaa 1314

<210> 44
 <211> 438
 <212> PRT
 <213> Synechocystis PCC6803

<400> 44

Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile
 1 5 10 15
 Tyr Trp Asp Ser Ile Val Pro Ile Thr Glu Thr Gly Val Glu Glu Val
 20 25 30
 Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile
 35 40 45
 Ile Val His Asn Ser Glu Glu Asp Leu Gly Ser Ser Val Gln Leu Ala
 50 55 60
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 65 70 75 80
 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
 85 90 95
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
 100 105 110
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Gly Ser Asn Gly Glu
 115 120 125
 Phe Ser Gln Val Asp Lys Ser Met Val Ser Lys Gly Glu Glu Leu Phe
 130 135 140
 Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly
 145 150 155 160
 His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly
 165 170 175
 Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro
 180 185 190
 Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser
 195 200 205
 Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met
 210 215 220

Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly
 225 230 235 240

Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val
 245 250 255

Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile
 260 265 270

Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile
 275 280 285

Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg
 290 295 300

His Asn Ile Glu Asp Leu Glu Gln Lys Leu Ile Cys Ile Ser Gly Asp
 305 310 315 320

Ser Leu Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp
 325 330 335

Leu Leu Asp Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr
 340 345 350

Met Lys Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys
 355 360 365

Lys Leu Val Tyr Ile Leu Lys Thr Arg Leu Gly Arg Thr Ile Lys Ala
 370 375 380

Thr Ala Asn His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp
 385 390 395 400

Glu Leu Ser Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser
 405 410 415

Ser Ser Leu Gln Leu Gly Leu Arg Gly Gln Tyr Pro Tyr Asp Val Pro
 420 425 430

Asp Tyr Ala Ile Asp Glx
 435

<210> 45

<211> 1314
 <212> DNA
 <213> Synechocystis PCC6803

<400> 45
 atggagtcgc gatcaccaga aatagaaaag ttgtctcaga gtgatattta ctgggactcc 60
 atcgttttcta ttacggagac tggagtcgaa gaggtttttg atttgactgt gccagggccc 120
 cataactttg tggccaatga catcattgtc cataacagtg aggaggacct gggatccagc 180
 gtgcagctcg ccgaccacta ccagcagaac acccccatcg gcgacggccc cgtgctgctg 240
 cccgacaacc actacctgag caccagtcgc gccctgagca aagaccccaa cgagaagcgc 300
 gatcacatgg tcctgctgga gttcgtgacc gccgccggga tcaactctcg catggacgag 360
 ctgtacaagg ggtcgaacgg ggaattctcg caggtagaca agtcgatggg gagcaagggc 420
 gaggagctgt tcaccggggg ggtgcccatc ctggtcgagc tggacggcga cgtaaacggc 480
 cacaagttca gcgtgtccgg cgagggcgag ggcgatgcc cctacggcaa gctgacctg 540
 aagttcatct gcaccaccgg caagctgccc gtgccctggc ccacctcgt gaccacctg 600
 acctacggcg tgcagtgtt cagccgctac cccgaccaca tgaagcagca cgactttctc 660
 aagtccgcca tgcccgaagg ctacgtccag gagcgcacca tcttcttcaa ggacgacggc 720
 aactacaaga cccgcgccga ggtgaagttc gagggcgaca ccctggtgaa ccgcatcgag 780
 ctgaagggca tcgacttcaa ggaggacggc aacatcctgg ggcacaagct ggagtacaac 840
 tacaacagcc acaacgtcta tatcatggcc gacaagcaga agaacggcat caaggtgaac 900
 ttcaagatcc gccacaacat cgaggacctc gagcaaaagc tgatatgcat ctccggagat 960
 agtttgatca gcttggcgag cacaggaaaa agagtttcta ttaaagattt gttagatgaa 1020
 aaagattttg aaatatgggc agttaatgaa cagacgatga agctagaatc agctaaagtt 1080
 agtcgtgtat tttgtactgg caaaaagcta gtttatattt taaaaactcg actaggtaga 1140
 actatcaagg caacagcaaa tcatagattt ttaactattg atgggttgaa aagattagat 1200
 gagctatctt taaaagagca tattgctcta ccccgtaaac tagaaagctc ctctttacaa 1260
 ttaggcctcc gcggccagta ccctacgac gtcccgact acgctatcga ttaa 1314

<210> 46
 <211> 438
 <212> PRT
 <213> Synechocystis PCC6803

<400> 46

Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile
 1 5 10 15

Tyr Trp Asp Ser Ile Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val
 20 25 30

Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile
 35 40 45

Ile Val His Asn Ser Glu Glu Asp Leu Gly Ser Ser Val Gln Leu Ala
 50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 65 70 75 80

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
 85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
 100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Gly Ser Asn Gly Glu
 115 120 125

Phe Ser Gln Val Asp Lys Ser Met Val Ser Lys Gly Glu Glu Leu Phe
 130 135 140

Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly
 145 150 155 160

His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly
 165 170 175

Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro
 180 185 190

Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser
 195 200 205

Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met
 210 215 220

Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly

225		230		235		240
Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val						
	245		250		255	
Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile						
	260		265		270	
Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile						
	275		280		285	
Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg						
	290		295		300	
His Asn Ile Glu Asp Leu Glu Gln Lys Leu Ile Cys Ile Ser Gly Asp						
	305		310		315	320
Ser Leu Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp						
		325		330		335
Leu Leu Asp Glu Lys Asp Phe Glu Ile Trp Ala Val Asn Glu Gln Thr						
	340		345		350	
Met Lys Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys						
	355		360		365	
Lys Leu Val Tyr Ile Leu Lys Thr Arg Leu Gly Arg Thr Ile Lys Ala						
	370		375		380	
Thr Ala Asn His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp						
	385		390		395	400
Glu Leu Ser Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser						
		405		410		415
Ser Ser Leu Gln Leu Gly Leu Arg Gly Gln Tyr Pro Tyr Asp Val Pro						
	420		425		430	
Asp Tyr Ala Ile Asp Glx						
	435					

<210> 47
 <211> 2043

<212> DNA
 <213> Synechocystis PCC6803

<220>
 <221> CDS
 <222> (739) .. (2043)
 <223>

<400> 47
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 gtaatcaatt acgggggtcat tagttcatag cccatatatg gagttccgcg ttacataact 120
 tacggtaaatt ggcccgctg gctgaccgcc caacgacccc cgccattga cgtcaataat 180
 gacgtatgtt cccatagtaa cgccaatagg gactttccat tgacgtcaat ggggtggacta 240
 ttacggtaa actgcccact tggcagtaca tcaagtgtat catatgccaa gtacgcccc 300
 tattgacgtc aatgacggt aatggccgc ctggcattat gccagtaca tgacctatc 360
 ggactttcct acttggcagt acatctacgt attagtcac gctattacca tggatgatgcg 420
 gttttggcag tacatcaatg ggcgtggata gcggtttgac tcacggggat ttccaagtct 480
 ccacccatt gacgtcaatg ggagtttgtt ttggcaccaa aatcaacggg actttccaaa 540
 atgtcgtaac aactccgcc cattgacgca aatgggcggt aggcgtgtac ggtgggaggt 600
 ctatataagc agagctctct ggctaactag agaaccact gcttactggc ttatcgaaat 660
 taatacgact cactataggg agaccaagc tggctagtta agcttcctag actaggagat 720
 ctgtcgactg gaggaacc atg gag tcc gga tca cca gaa ata gaa aag ttg 771
 Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu
 1 5 10
 tct cag agt gat att tac tgg gac tcc atc gtt tct att acg gag act 819
 Ser Gln Ser Asp Ile Tyr Trp Asp Ser Ile Val Ser Ile Thr Glu Thr
 15 20 25
 gga gtc gaa gag gtt ttt gat ttg act gtg cca gga cca cat aac ttt 867
 Gly Val Glu Glu Val Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe
 30 35 40
 gtc gcc aat gac atc att gtc cat aac agt atc gaa caa ggc cag ggc 915
 Val Ala Asn Asp Ile Ile Val His Asn Ser Ile Glu Gln Gly Gln Gly
 45 50 55
 ggt ggc atg tca atg gac tat aaa gat gac gac gat aag atg agg atg 963
 Gly Gly Met Ser Met Asp Tyr Lys Asp Asp Asp Asp Lys Met Arg Met
 60 65 70 75
 ctc gag ggc caa gca ggt gga ctg atc acc agt ggc tgc atc agt gga 1011
 Leu Glu Gly Gln Ala Gly Gly Leu Ile Thr Ser Gly Cys Ile Ser Gly
 80 85 90

gat agt ttg atc agc ttg gcg agc aca gga aaa aga gtt tct att aaa	1059
Asp Ser Leu Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys	
95 100 105	
gat ttg tta gat gaa aaa gat ttt gaa ata tgg gca att aat gaa cag	1107
Asp Leu Leu Asp Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln	
110 115 120	
acg atg aag cta gaa tca gct aaa gtt agt cgt gta ttt tgt act ggc	1155
Thr Met Lys Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly	
125 130 135	
aaa aag cta gtt tat att tta aaa act cga cta ggt aga act atc aag	1203
Lys Lys Leu Val Tyr Ile Leu Lys Thr Arg Leu Gly Arg Thr Ile Lys	
140 145 150 155	
gca aca gca aat cat aga ttt tta act att gat ggt tgg aaa aga tta	1251
Ala Thr Ala Asn His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu	
160 165 170	
gat gag cta tct tta aaa gag cat att gct cta ccc cgt aaa cta gaa	1299
Asp Glu Leu Ser Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu	
175 180 185	
agc tcc tct tta caa tta atc gat atg gtg agc aag ggc gag gag ctg	1347
Ser Ser Ser Leu Gln Leu Ile Asp Met Val Ser Lys Gly Glu Glu Leu	
190 195 200	
ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg gac ggc gac gta aac	1395
Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn	
205 210 215	
ggc cac aag ttc agc gtg tcc ggc gag ggc gag ggc gat gcc acc tac	1443
Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr	
220 225 230 235	
ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg	1491
Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val	
240 245 250	
ccc tgg ccc acc ctg gtg acc acc ctg acc tac ggc gtg cag tgc ttc	1539
Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe	
255 260 265	
agc cgc tac ccc gac cac atg aag cag cac gac ttc ttc aag tcc gcc	1587
Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala	
270 275 280	
atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac	1635
Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp	
285 290 295	
ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg	1683
Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu	
300 305 310 315	

gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac 1731
 Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
 320 325 330

 atc ctg ggg cac aag ctg gag tac aac tac aac agc cac aac gtc tat 1779
 Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
 335 340 345

 atc atg gcc gac aag cag aag aac ggc atc aag gtg aac ttc aag atc 1827
 Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
 350 355 360

 cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag 1875
 Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
 365 370 375

 cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac 1923
 Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
 380 385 390 395

 tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc 1971
 Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
 400 405 410

 gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc 2019
 Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
 415 420 425

 ggc atg gac gag ctg tac aag taa 2043
 Gly Met Asp Glu Leu Tyr Lys
 430

<210> 48
 <211> 434
 <212> PRT
 <213> Synechocystis PCC6803

<400> 48

Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile
 1 5 10 15

Tyr Trp Asp Ser Ile Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val
 20 25 30

Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile
 35 40 45

Ile Val His Asn Ser Ile Glu Gln Gly Gln Gly Gly Gly Met Ser Met
 50 55 60

Asp Tyr Lys Asp Asp Asp Asp Lys Met Arg Met Leu Glu Gly Gln Ala

65		70		75		80
Gly Gly Leu Ile Thr Ser Gly Cys Ile Ser Gly Asp Ser Leu Ile Ser						
	85			90		95
Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp Leu Leu Asp Glu						
	100			105		110
Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys Leu Glu						
	115			120		125
Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys Lys Leu Val Tyr						
	130			135		140
Ile Leu Lys Thr Arg Leu Gly Arg Thr Ile Lys Ala Thr Ala Asn His						
	145			150		155
						160
Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp Glu Leu Ser Leu						
				165		170
						175
Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser Ser Ser Leu Gln						
	180			185		190
Leu Ile Asp Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val						
	195			200		205
Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser						
	210			215		220
Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu						
	225			230		235
						240
Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu						
				245		250
						255
Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp						
	260			265		270
His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr						
	275			280		285
Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr						
	290			295		300

Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
305 310 315 320

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys
325 330 335

Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys
340 345 350

Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
355 360 365

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
370 375 380

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
385 390 395 400

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
405 410 415

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
420 425 430

Tyr Lys

<210> 49
<211> 437
<212> PRT
<213> Artificial sequence

<220>
<223> DnaB intein cyclization scaffold with GFP

<400> 49

Met Glu Ser Gly Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile
1 5 10 15

Tyr Trp Asp Ser Ile Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val
20 25 30

Phe Asp Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile

35

40

45

Ile Val His Asn Ser Glu Glu Asp Leu Gly Ser Ser Val Gln Leu Ala
 50 55 60

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 65 70 75 80

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
 85 90 95

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
 100 105 110

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Gly Ser Asn Gly Glu
 115 120 125

Phe Ser Gln Val Asp Lys Ser Met Val Ser Lys Gly Glu Glu Leu Phe
 130 135 140

Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly
 145 150 155 160

His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly
 165 170 175

Leu Lys Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro
 180 185 190

Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Leu Gln Cys Phe Ser
 195 200 205

Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met
 210 215 220

Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly
 225 230 235 240

Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val
 245 250 255

Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile
 260 265 270

Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile
275 280 285

Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg
290 295 300

His Asn Ile Glu Asp Leu Glu Gln Lys Leu Ile Cys Ile Ser Gly Asp
305 310 315 320

Ser Leu Ile Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp
325 330 335

Leu Leu Asp Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr
340 345 350

Met Lys Leu Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys
355 360 365

Lys Leu Val Tyr Ile Leu Lys Thr Arg Leu Gly Arg Thr Ile Lys Ala
370 375 380

Thr Ala Asn His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp
385 390 395 400

Glu Leu Ser Lys Leu Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser
405 410 415

Ser Ser Leu Gln Leu Gly Leu Arg Gly Gln Tyr Pro Tyr Asp Val Pro
420 425 430

Asp Tyr Ala Ile Asp
435

<210> 50
<211> 5
<212> PRT
<213> Unknown

<220>
<223> fragment of myc epitope

<400> 50

Ser Glu Glu Asp Leu

1 5

<210> 51
<211> 5
<212> PRT
<213> Unknown

<220>
<223> fragment of myc epitope

<400> 51

Glu Gln Lys Leu Ile
1 5

<210> 52
<211> 23
<212> PRT
<213> Artificial sequence

<220>
<223> fragment from cyclized GFP and reconstructed myc epitope

<400> 52

His Asn Ile Glu Asp Leu Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10 15

Gly Ser Ser Val Gln Leu Ala
20

<210> 53
<211> 5
<212> PRT
<213> Unknown

<220>
<223> fragment of myc epitope

<400> 53

Leu Asp Glu Glu Ser
1 5

<210> 54
<211> 155
<212> PRT
<213> Synechocystis PCC6803

<400> 54

Cys Ile Ser Gly Asp Ser Leu Ile Ser Leu Ala Ser Thr Gly Lys Arg

1	5	10	15
Val Ser Ile Lys Asp Leu Leu Asp Glu Lys Asp Phe Glu Ile Trp Ala	20	25	30
Ile Asn Glu Gln Thr Met Lys Leu Glu Ser Ala Lys Val Ser Arg Val	35	40	45
Phe Cys Thr Gly Lys Lys Leu Val Tyr Ile Leu Lys Thr Arg Leu Gly	50	55	60
Arg Thr Ile Lys Ala Thr Ala Asn His Arg Phe Leu Thr Ile Asp Gly	65	70	75
Trp Lys Arg Leu Asp Glu Leu Ser Leu Lys Glu His Ile Ala Leu Pro	85	90	95
Arg Lys Leu Glu Ser Ser Ser Leu Gln Leu Ser Pro Glu Ile Glu Lys	100	105	110
Leu Ser Gln Ser Asp Ile Tyr Trp Asp Ser Ile Val Ser Ile Thr Glu	115	120	125
Thr Gly Val Glu Glu Val Phe Asp Leu Thr Val Pro Gly Pro His Asn	130	135	140
Phe Val Ala Asn Asp Ile Ile Val His Asn Ser	145	150	155
<210> 55			
<211> 199			
<212> PRT			
<213> Mycobacterium xenopi			
<400> 55			
Cys Ile Thr Gly Asp Ala Leu Val Ala Leu Pro Glu Gly Glu Ser Val	1	5	10
Arg Ile Ala Asp Ile Val Pro Gly Ala Arg Pro Asn Ser Asp Asn Ala	20	25	30
Ile Asp Leu Lys Val Leu Asp Arg His Gly Asn Pro Val Leu Ala Asp	35	40	45

Arg Leu Phe His Ser Gly Glu His Pro Val Tyr Thr Val Arg Thr Val
 50 55 60

Glu Gly Leu Arg Val Thr Gly Thr Ala Asn His Pro Leu Leu Cys Leu
 65 70 75 80

Val Asp Val Ala Gly Val Pro Thr Leu Leu Trp Lys Leu Ile Asp Glu
 85 90 95

Ile Lys Pro Gly Asp Tyr Ala Val Ile Gln Arg Ser Ala Phe Ser Val
 100 105 110

Asp Cys Ala Gly Phe Ala Arg Gly Lys Pro Glu Phe Ala Pro Thr Thr
 115 120 125

Tyr Thr Val Gly Val Pro Gly Leu Val Arg Phe Leu Glu Ala His His
 130 135 140

Arg Asp Pro Asp Ala Gln Ala Ile Ala Asp Glu Leu Thr Asp Gly Arg
 145 150 155 160

Phe Tyr Tyr Ala Pro Val Ala Ser Val Thr Asp Ala Gly Val Gln Pro
 165 170 175

Val Tyr Ser Leu Arg Val Asp Thr Ala Asp His Ala Phe Ile Thr Asn
 180 185 190

Gly Phe Val Ser His Asn Thr
 195

<210> 56
 <211> 20
 <212> PRT
 <213> Artificial sequence

<220>
 <223> reconstructed myc epitope with BstX I-Linker

<400> 56

Gly Gln Gly Gly Gly Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Gln
 1 5 10 15

Ala Gly Gly Gly
 20

<210> 57
<211> 7
<212> PRT
<213> Unknown

<220>
<223> cyclic peptide

<400> 57

Ser Arg Gly Asp Gly Trp Ser
1 5

<210> 58
<211> 9
<212> PRT
<213> Unknown

<220>
<223> cyclic peptide

<400> 58

Ser Gly Arg Gly Asp Gly Trp Gly Ser
1 5

<210> 59
<211> 7
<212> PRT
<213> Unknown

<220>
<223> cyclic peptide

<400> 59

Ser Arg Gly Pro Gly Trp Ser
1 5

<210> 60
<211> 7
<212> PRT
<213> Simian virus 40

<400> 60

Pro Lys Lys Lys Arg Lys Val
1 5

<210> 61
<211> 6

<212> PRT
<213> Homo sapiens

<400> 61

Ala Arg Arg Arg Arg Pro
1 5

<210> 62
<211> 10
<212> PRT
<213> Mus musculus

<400> 62

Glu Glu Val Gln Arg Lys Arg Gln Lys Leu
1 5 10

<210> 63
<211> 9
<212> PRT
<213> Mus musculus

<400> 63

Glu Glu Lys Arg Lys Arg Thr Tyr Glu
1 5

<210> 64
<211> 20
<212> PRT
<213> Xenopus laevis

<400> 64

Ala Val Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys
1 5 10 15

Lys Lys Leu Asp
20

<210> 65
<211> 31
<212> PRT
<213> Mus musculus

<400> 65

Met Ala Ser Pro Leu Thr Arg Phe Leu Ser Leu Asn Leu Leu Leu Leu
1 5 10 15

Gly Glu Ser Ile Leu Gly Ser Gly Glu Ala Lys Pro Gln Ala Pro
 20 25 30

<210> 66
 <211> 21
 <212> PRT
 <213> Homo sapiens

<400> 66

Met Ser Ser Phe Gly Tyr Arg Thr Leu Thr Val Ala Leu Phe Thr Leu
 1 5 10 15

Ile Cys Cys Pro Gly
 20

<210> 67
 <211> 51
 <212> PRT
 <213> Mus musculus

<400> 67

Pro Gln Arg Pro Glu Asp Cys Arg Pro Arg Gly Ser Val Lys Gly Thr
 1 5 10 15

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
 20 25 30

Ile Cys Val Ala Leu Leu Leu Ser Leu Ile Ile Thr Leu Ile Cys Tyr
 35 40 45

His Ser Arg
 50

<210> 68
 <211> 33
 <212> PRT
 <213> Homo sapiens

<400> 68

Met Val Ile Ile Val Thr Val Val Ser Val Leu Leu Ser Leu Phe Val
 1 5 10 15

Thr Ser Val Leu Leu Cys Phe Ile Phe Gly Gln His Leu Arg Gln Gln
 20 25 30

Arg

<210> 69
<211> 37
<212> PRT
<213> Rattus sp.

<400> 69

Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser
1 5 10 15

Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr
20 25 30

Met Gly Leu Leu Thr
35

<210> 70
<211> 14
<212> PRT
<213> Homo sapiens

<400> 70

Met Gly Ser Ser Lys Ser Lys Pro Lys Asp Pro Ser Gln Arg
1 5 10

<210> 71
<211> 26
<212> PRT
<213> Homo sapiens

<400> 71

Leu Leu Gln Arg Leu Phe Ser Arg Gln Asp Cys Cys Gly Asn Cys Ser
1 5 10 15

Asp Ser Glu Glu Glu Leu Pro Thr Arg Leu
20 25

<210> 72
<211> 20
<212> PRT
<213> Rattus norvegicus

<400> 72

Lys Gln Phe Arg Asn Cys Met Leu Thr Ser Leu Cys Cys Gly Lys Asn

1 5 10 15

Pro Leu Gly Asp
20

<210> 73
<211> 19
<212> PRT
<213> Homo sapiens

<400> 73

Leu Asn Pro Pro Asp Glu Ser Gly Pro Gly Cys Met Ser Cys Lys Cys
1 5 10 15

Val Leu Ser

<210> 74
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> lysosomal degradation sequence

<400> 74

Lys Phe Glu Arg Gln
1 5

<210> 75
<211> 36
<212> PRT
<213> Cricetulus griseus

<400> 75

Met Leu Ile Pro Ile Ala Gly Phe Phe Ala Leu Ala Gly Leu Val Leu
1 5 10 15

Ile Val Leu Ile Ala Tyr Leu Ile Gly Arg Lys Arg Ser His Ala Gly
20 25 30

Tyr Gln Thr Ile
35

<210> 76
<211> 35

<212> PRT
<213> Homo sapiens

<400> 76

Leu Val Pro Ile Ala Val Gly Ala Ala Leu Ala Gly Val Leu Ile Leu
1 5 10 15

Val Leu Leu Ala Tyr Phe Ile Gly Leu Lys His His His Ala Gly Tyr
20 25 30

Glu Gln Phe
35

<210> 77
<211> 27
<212> PRT
<213> Yeast

<400> 77

Met Leu Arg Thr Ser Ser Leu Phe Thr Arg Arg Val Gln Pro Ser Leu
1 5 10 15

Phe Ser Arg Asn Ile Leu Arg Leu Gln Ser Thr
20 25

<210> 78
<211> 25
<212> PRT
<213> Yeast

<400> 78

Met Leu Ser Leu Arg Gln Ser Ile Arg Phe Phe Lys Pro Ala Thr Arg
1 5 10 15

Thr Leu Cys Ser Ser Arg Tyr Leu Leu
20 25

<210> 79
<211> 64
<212> PRT
<213> Yeast

<400> 79

Met Phe Ser Met Leu Ser Lys Arg Trp Ala Gln Arg Thr Leu Ser Lys
1 5 10 15

Ser Phe Tyr Ser Thr Ala Thr Gly Ala Ala Ser Lys Ser Gly Lys Leu
 20 25 30

Thr Gln Lys Leu Val Thr Ala Gly Val Ala Ala Ala Gly Ile Thr Ala
 35 40 45

Ser Thr Leu Leu Tyr Ala Asp Ser Leu Thr Ala Glu Ala Met Thr Ala
 50 55 60

<210> 80
 <211> 41
 <212> PRT
 <213> Yeast

<400> 80

Met Lys Ser Phe Ile Thr Arg Asn Lys Thr Ala Ile Leu Ala Thr Val
 1 5 10 15

Ala Ala Thr Gly Thr Ala Ile Gly Ala Tyr Tyr Tyr Tyr Asn Gln Leu
 20 25 30

Gln Gln Gln Gln Gln Arg Gly Lys Lys
 35 40

<210> 81
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 81

Lys Asp Glu Leu
 1

<210> 82
 <211> 15
 <212> PRT
 <213> unidentified adenovirus

<400> 82

Leu Tyr Leu Ser Arg Arg Ser Phe Ile Asp Glu Lys Lys Met Pro
 1 5 10 15

<210> 83
 <211> 19
 <212> PRT

<213> Homo sapiens

<400> 83

Leu Asn Pro Pro Asp Glu Ser Gly Pro Gly Cys Met Ser Cys Lys Cys
1 5 10 15

Val Leu Ser

<210> 84

<211> 15

<212> PRT

<213> Homo sapiens

<400> 84

Leu Thr Glu Pro Thr Gln Pro Thr Arg Asn Gln Cys Cys Ser Asn
1 5 10 15

<210> 85

<211> 9

<212> PRT

<213> Unknown

<220>

<223> cyclin B1 destruction sequence

<400> 85

Arg Thr Ala Leu Gly Asp Ile Gly Asn
1 5

<210> 86

<211> 20

<212> PRT

<213> Unknown

<220>

<223> signal sequence from Interleukin-2

<400> 86

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1 5 10 15

Val Thr Asn Ser
20

<210> 87

<211> 29

<212> PRT
<213> Homo sapiens

<400> 87

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1 5 10 15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr
20 25

<210> 88
<211> 27
<212> PRT
<213> Homo sapiens

<400> 88

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
1 5 10 15

Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn
20 25

<210> 89
<211> 18
<212> PRT
<213> Influenza virus

<400> 89

Met Lys Ala Lys Leu Leu Val Leu Leu Tyr Ala Phe Val Ala Gly Asp
1 5 10 15

Gln Ile

<210> 90
<211> 24
<212> PRT
<213> Unknown

<220>
<223> signal sequence from Interleukin-4

<400> 90

Met Gly Leu Thr Ser Gln Leu Leu Pro Pro Leu Phe Phe Leu Leu Ala
1 5 10 15

Cys Ala Gly Asn Phe Val His Gly
20